

Result No.	Score	Query Match	Length	DB ID	Description
1	1789	61.1	383	4	US-09-149-476-460 Sequence 460, App
2	136	4.6	591	4	US-09-236-540-2490 Sequence 2490, Ap
3	123.5	4.2	524	2	US-08-938-692-12 Sequence 12, App
4	123.5	4.2	524	4	US-09-339-977-12 Sequence 12, App
5	117	4.0	490	1	US-09-489-032A-1322 Sequence 1322, A
6	113.5	3.9	329	4	US-09-489-032A-1420 Sequence 1420, A
7	112	3.8	305	4	US-09-236-392A-1406 Sequence 33032, A
8	110	3.8	352	4	US-09-328-352A-4392 Sequence 4392, Ap
9	109.5	3.7	470	4	US-09-134-001C-4610 Sequence 4610, Ap
10	108	3.7	330	1	US-08-118-270-19 Sequence 19, App
11	108	3.7	330	5	PCT-US93-08528-19 Sequence 19, App
12	108	3.7	549	4	US-09-489-032A-8237 Sequence 8237, Ap
13	108	3.7	618	4	US-08-589-552A-2 Sequence 2, Appli
14	108	3.7	618	4	US-09-560-198D-4 Sequence 4, Appli
15	107.5	3.7	491	4	US-09-541-68IA-8251 Sequence 8251, Ap
16	107.5	3.7	897	4	US-09-553-68IA-4229 Sequence 4229, Ap
17	107	3.7	411	4	US-09-134-001C-3389 Sequence 3299, Ap
18	107	3.7	465	4	US-09-328-352A-5222 Sequence 5222, Ap
19	107	3.7	512	4	US-09-541-236-3548 Sequence 3548, Ap
20	104	3.6	534	2	US-09-031-392A-4 Sequence 4, Appli
21	104	3.6	534	3	US-09-239-549-4 Sequence 4, Appli
22	104	3.6	534	4	US-09-611-417-4 Sequence 4, Appli
23	103.5	3.5	471	4	US-09-322-314-17 Sequence 17, Appli
24	103	3.5	358	2	US-08-718-485-6 Sequence 6, Appli
25	103	3.5	443	4	US-09-651-960-3 Sequence 3, Appli
26	102.5	3.5	443	4	US-08-658-332B-33 Sequence 33, Appli
27	102.5	3.5	529	4	US-09-406-640-33 Sequence 33, Appli

ALIGNMENTS

RESULT 1
US-09-119-476-460 ; Sequence 460, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23

1 EARLIER APPLICATION NUMBER: 60/047,500
1 EARLIER FILING DATE: 1997-05-3
1 EARLIER APPLICATION NUMBER: 60/047,587
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,492
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,598
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,613
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,582
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,596
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,612
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,580
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,632
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,601
1 EARLIER FILING DATE: 1997-05-23
1 EARLIER APPLICATION NUMBER: 60/047,611
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,568
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,314
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,569
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,311
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,314
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,674
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,669
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,312
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,313
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,672
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,315
1 EARLIER FILING DATE: 1997-04-11
1 EARLIER APPLICATION NUMBER: 60/043,974
1 EARLIER FILING DATE: 1997-06-06
1 EARLIER APPLICATION NUMBER: 60/056,886
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,877
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,889
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,893
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,630
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,882
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,637
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,903
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,888
1 EARLIER FILING DATE: 1997-08-22
1 EARLIER APPLICATION NUMBER: 60/056,879
1 EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 61.1%; Score 1789; DB 4; Length 383;
 Best Local Similarity 92.4%; Pred. No. 9.9e-175;
 Matches 353; Conservative 3; Mismatches 26; Indels 0; Gaps 0;

Qy 190 NAVGQINTMFGSPVIGCFISGNLVSMCVEYLLMKVQTKPALAVKAGIKEEETELQL 249
 Db 1 NAVGQINTMFGSPVIGCFISGNLVSMCVEYLLMKVQTKPALAVKAGIKEEETELQL 60

Qy 250 NHKDKTEPKPLEGTHMGVDSNTHLEHEBPTCSQAEPEFRDGVSYNQPVL 309
 Db 61 NHKDKTEPKPLEGTHMGVDSNTHLEHEBPTCSQAEPEFRDGVSYNQPVL 120

Qy 310 AGMGLAFLYMTVLGFDCITGGAYATGSGSILSILMGASAITGIMGTVAFTWLRRKG 369
 Db 121 AGMGLAFLYMTVLGFDCITGGAYATGSGSILSILMGASAITGIMGTVAFTWLRRKG 180

Qy 370 VRTGLISGLAQSLCLCVISVMPGSPLDLSVSPPEDIRSREIOGESITPTKIPETIE 429
 Db 181 GSAGLISGLAQSLCLCVISVMPGSPLDLSVSPPEDIRSREIOGESITPTKIPETIE 240

Qy 430 TYMSNGNSANIVPETSPESPVSLSLFAGVIAARGLNSFDLTVTQLQENVIESTER 489
 Db 241 TYMSNGNSANIVPETSPESPVSLSLFAGVIAARGLNSFDLTVTQLQENVIESTER 300

Qy 490 GLINGVONSMYLLDLHFINVYLAPNEAFLGLVLIISFSVAMGHIMYRFAQNTLGRK 549
 Db 301 GLINGVONSMYLLDLHFINVYLAPNEAFLGLVLIISFSVAMGHIMYRFAQNTLGRK 360

Qy 550 LFACGPDAKEVKRNQNTSVV 571
 Db 361 LFACGPDAKEVKRNQNTSVV 382

RESULT 2
 US-09-540-216-2490
 ; Sequence 2490, Application US/09540236
 ; Patent No 6673910
 ; GENERAL INFORMATION
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAKELLA CATAR
 ; FILE REFERENCE: 2709-2005-0015
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 2490
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: M.catarrhalis
 US-09-540-216-2490

Query Match 4.6%; Score 136; DB 4; Length 591;
 Best Local Similarity 19.2%; Pred. No. 6.3e-05;
 Matches 120; Conservative 94; Mismatches 228; Indels 182; Gaps 27;
 Qy 18 ADLTSAKPLLYGHSLSTWGDRMMHFAVSVLV-----51

Db 52 ADMSAAFISWAG-MIAGG----YAASATIMGHTGGFVILLALAPYLRKGFFTPV 105
 Qy 52 -----ELYGNSSLTAVGLVVAQSVLGAIGDWYDNARLKV-AQTSLVQVQNSVIL 105
 Db 106 DFIGDRFSKTAIRAVVCLILACTIVGQNTGAGVAFSLEVDTSNTGLIIRALVLF 165
 Qy 106 CGTIIIMM--VFUJKHELTUHMWGVJLITIANLASTATAITIQ 155
 Db 166 YAVLGGMGKITYTQVAQCVLMVAYIIFAIISLNLTGNPPIQLGMEGNDVSTGMBILQK 225

Qy 156 RDWIVVAGEDRSKLAMNATIRRQDQLTNILAPNAVGQINTFGSPVIGCFI-----208
 Db 226 LDMLVADIG----FQXTADVP--NKLNMFLTM-S-MICTAGLFLVIRFFTEKVSD 277
 Qy 209 ----SGNLVSMCVEYLLMKVQTKPALAVKAGIKEEET---EIKQLNQHJDTEP---257
 Db 278 ARISAGWTLIFIAL----LYTTAPAVGSMARLNINTVYPQGINQPALAYEARPEWM 330

Qy 268 KPLGEHTHMGVDSNTHELEHQEPQTCASQAEPPTRDGEWSYNQPVFLAGMGAFL 317
 Db 331 KWEETGULLKYEDKN-----NDGLIQQNDK-----NST 356

Qy 318 YMTVLFDFCITGGAYAT----QGLSSSILS----ILMGASAITGIMGTVAFTWLRRKG 368

Db 357 -----NEYATIVTAEGWQGNELIANDIVLANPEANI-----SWV---IG 398

Qy 369 LVRTGLISGLAQSLCLCVISVMPGSPLDLSVSPPEDIRSREFGESETPTKIPETIE 428
 Db 399 LIAAGLAAALSTAGLLAISAISSHLIRKTIK-P-DINDK--GELMARISITIAI 453

Db 429 ELINNSGNSANIVPETSPESPVSL-----LFGVIAARIGLWSFDLTVQLOENV 485

Qy 454 VVATYLGNNPPGFTAAQVVAFSGIASSLFPALMGMGFSRKI-----NST 498

Qy 486 ESRGTINGVQNEMNYLLDLHFMVILAP-----NPEAFLLVLLISFSVAMGHIMYF 539

Db 499 GRTAGMIGLSATCITYFLYNGMFPI----PGTNSFVNEAHLGSPLSFGAVINE 555

Qy 540 --RFAQNTLGNKLFACGPDAKEVR 561

Db 556 IVAIATVSAANGN----PPREVQ .573

RESULT 3
 US-08-938-692-12
 ; Sequence 12, Application US/08928692
 ; Patent No. 5958727
 ; GENERAL INFORMATION:
 ; APPLICANT: Brody, Howard S.
 ; APPLICANT: Yaver, Deborah S.
 ; APPLICANT: Lamsa, Michael
 ; APPLICANT: Hansen, Kim
 ; TITLE OF INVENTION: Methods for Modifying the Production of
 ; NUMBER OF SEQUENCES: 80
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSE: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/928,692
 ; FILING DATE: 12-SEPT-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 4944-200-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-878-9655
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 524 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
 TOPOLGY: linear
 MOLECULE TYPE: No. 595872e
 US-09-928-692-12

Query Match 4.2%; Score 123.5; DB 2; Length 524;
 Best Local Similarity 20.3%; Pred. No. 0.001; Gaps 23;
 Matches 99; Conservative 69; Mismatches 150; Indels 169; Gaps 23;

Query 41 MNHFAVSVYEL--ELYGNSL--LUTAVGLWVAGSVLVLYGALIIGDWYDKNARLKVAQ 93
 Db 96 LWSLSVSSPAVGCMTAFFGGMGLDTIGRKAMLVANILSVLGALLMGF----SKLGP 149

Query 94 TSLVV---QNSVILCGGILMMVFELKHKEIITMYHGWLSCYLITIANIANIASTAT 150
 Db 150 SHIIAGRSISLYCGI-----SGLYEMY-----IGEAPTA- 183

Query 151 AIIIQDRWIVVVAEGDRSKLAMNATIRRIDLNTILAPKAVGQIMTFGGSPVIGCFISG 210
 Db 184 -----LRLGALGPFPHQIAVTGIL-----SQQIGLEFILG 213

Query 211 ----WNL-----VSMCVYEYLJLWKTYQKTPALAVKAGLKEBETELKQLMLHKDTEPKPL 260
 Db 214 NYDLWHILLGLSGVRAILQSLIIFCPESPRYLYKL---DEEVRAKO-SLKR----- 262

Query 261 EGTHLMGVRD--SNIHBLHEDEOPTCASQMEPFRFRDGWVSYNNQPvFLAGM-GLAFL 317
 Db 263 ---LRGYDDTKDINEMRKEEREAESSEQKVSIQIQLFTN--SSYRQPIILVALMLHVAOQ 315

Query 318 YMTVLGFPCIDTGYAYTQQLGSSILSILMGAASAITGIMTVAAFTWLRRKGGLVRTGLISG 377
 Db 316 FSGINGIFYYSTSFQTAGISKPVYATI-GVGAANNVF-TAVSVLVEKAQRSLFLIGM 373

Query 378 LAQSLCLI-----LCVVISVMPGSPLDLVSPPEDIRSRIQGESTP 420
 Db 374 SGMFVCATFMSVGLVLINKFSMSVSMIA.F-----LFVSEFFE-----TGP 415

Query 421 TKIPEITTEIYMSNGNSNSANIVPETSPEVPIIS-----YSIL 458
 Db 416 GP!PWFENVAEFPFSQG-----PRPAALAAIAAFSNWTNCNPIVALCFQYIAADFCGPYVFFL 468

Query 459 FAVVIA 465
 Db 469 FAVVLLA 475

RESULT 4
 US-09-339-972-12
 ; Sequence 1.2, Application US/09339972
 ; GENERAL INFORMATION:
 ; APPLICANT: Brody, Howard
 ; APPLICANT No. 6323002
 ; APPLICANT: Yaver, Deborah S.
 ; APPLICANT: Lamia, Michael
 ; APPLICANT: Hansen, Kim
 ; TITLE OF INVENTION: Methods for Modifying the Production of
 ; NUMBER OF SEQUENCES: 80
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/339, 972
 ; FILING DATE:

CLASSIFICATION:
 PRIORITY APPLICATION DATA: 08/928, 692
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 4944.200-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-878-9655
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 524 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: No. 6323002e
 US-09-339-972-12

Query Match 4.2%; Score 123.5; DB 4; Length 524;
 Best Local Similarity 20.3%; Pred. No. 0.001;
 Matches 99; Conservative 69; Mismatches 150; Indels 169; Gaps 23;

Query 41 MNHFAVSVYEL--ELYGNSL--LUTAVGLWVAGSVLVLYGALIIGDWYDKNARLKVAQ 93
 Db 96 LWSLSVSSPAVGCMTAFFGGMGLDTIGRKAMLVANILSVLGALLMGF----SKLGP 149

Query 94 TSLVV--QNSVILCGGILMMVFELKHKEIITMYHGWLSCYLITIANIANIASTAT 150
 Db 150 SHIIAGRSISLYCGI-----SGLYEMY-----IGEAPTA- 183

Query 151 AIIIQDRWIVVVAEGDRSKLAMNATIRRIDLNTILAPKAVGQIMTFGGSPVIGCFISG 210
 Db 184 -----LRLGALGPFPHQIAVTGIL-----SQQIGLEFILG 213

Query 211 ----WNL-----VSMCVYEYLJLWKTYQKTPALAVKAGLKEBETELKQLMLHKDTEPKPL 260

Query 261 EGTHLMGVKD--SNIHELEHEOPTCASQMEPFRFRDGWVSYNNQPvFLAGM-GLAFL 317
 Db 263 ---NRGYDDTKDINEMRKEEREAESSEQKVSIQIQLFTN--SSYRQPIILVALMLHVAOQ 315

Query 318 YMTVLGFPCIDTGYAYTQQLGSSILSILMGAASAITGIMTVAAFTWLRRKGGLVRTGLISG 377
 Db 316 FSGINGIFYYSTSFQTAGISKPVYATI-GVGAANNVF-TAVSVLVEKAQRSLFLIGM 373

Query 378 LAQSLCLI-----LCVVISVMPGSPLDLVSPPEDIRSRIQGESTP 420
 Db 374 SGMFVCATFMSVGLVLINKFSMSVSMIA.F-----LFVSEFFE-----TGP 415

Query 421 TKIPEITTEIYMSNGNSNSANIVPETSPEVPIIS-----YSIL 458
 Db 416 GP!PWFENVAEFPFSQG-----PRPAALAAIAAFSNWTNCNPIVALCFQYIAADFCGPYVFFL 468

Query 459 FAVVIA 465
 Db 469 FAVVLLA 475

RESULT 5
 US-09-489-039A-13226
 ; Sequence 13226, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709-2004001
 ; CURRENT APPLICATION NUMBER: US/09/489, 039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIORITY APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13225
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13226

Query Match 4.0%; Score 117; DB 4; Length 490;
Best Local Similarity 18.5%; Pred. No. 0.0042;
Matches 95; Conservative 62; Mismatches 138; Indels 218; Gaps 25;

Qy 3 RAGDEHRQRGCGCSLADYLTSAKFLLYGHSLSTGDRWHAEVN----- 54
Db 9 RRADEN---CCDSL-----ISIEGTMQ-AILSFTEIFSQPAFLMG 47
Qy 55 -----GNSIL-----LTAVYGLVVA-----GSVIVLGATIGDWDY 84
Db 48 LIAFVGIVALRSPGNKLTTGTLKPIGLYMLASAGVVANLNPLGGIEAGFNTRGVIP 107
Qy 85 XN-ARLKVAQCSLVVQNVSILVSVLCLIMMVEL---HKEHLLTMHGWVLTSCYLITI 139
Db 108 NNEAIVSVAQKMLGVTMSILGFIFNLITIARCTPKYKTFLGHSHFACLSAVLOA 167
Qy 140 ANIANLSSATAITIQRDWIVVAGEDRSKLANNMATTIRIDQLTNLAPMAVGQIMTG 199
Db 168 AEF-----QGMLLIG---- 179
Qy 200 SPVIGCGTISG-WNLVSMCVEYVLLMRVQKTPALAVAGLKEETEELLKOLNLHKDTEPK 258
Db 180 -----GFLGWSMAs-----PAIG---- 203
Qy 259 PLEGTHMLGKDSNTHEHEQPTCASQMAEPFRTRDGWVS---YNQPVFLAGMGL 314
Db 204 -----DG-----GIANGHFGSGLYLISAWATARTNPANSFADEISEKNGFLRDTTFTG-- 254
Qy 315 AFLYMTVLGFDC-ITTCYAYTOGLSGS---ILSILMGASALTGNGTVAFTWLRRKGGLV 370
Db 255 --IVMFYTFVCSAVAGSAYLSTITDNLMLFSLQFAGV--AIVNGVR---- 304
Qy 371 RTGLISIAGLQLCILCVISMPGSPLDVSPEFDIERSFIQESITITPKBITEI 430
Db 305 --LILG-----DL-VPAFGISQKL-----PDSIPAVDCAV 333
Qy 431 YMSNGNSNANIVPETSPSVPVLISSVSLPAGV 463
Db 334 FFT-----FSPTAVVGFISSEFGGIV 355

RESULT 6
US-09-489-039A-14206
; Sequence 14206, Application US/09489039A
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-09
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14206
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14206

Query Match 3.9%; Score 113.5; DB 4; Length 329;
Best Local Similarity 20.1%; Pred. No. 0.005; Mismatches 133; Indels 123; Gaps 15;

Qy 45 AVSVELVLYGNSSLTAVYGLVVAASVVLGAIIQGDWVDKNARLKVAFTSLVWVONVSVI 104
Db 25 ANTAFLQQLNGLTLAVGJIAIGYTMVIG-IIG-----MINFAHGE--VVMVSAV 74
Qy 105 LC-GILLMMVF LHKEHLL-----TMYHGKVLTSCYLITIANTIANLASTAT 150
Db 75 LCAIGLALLSFFGITHSPFLLIFATLVTIVTGIVWAIER--IAYRPLRSTRLPLIS 132
Qy 151 AI---TQDWMIVVAAEDRSKLANNMATTIRIDQLTNLAPMAVGQIMTGSPVIGCGF 207
Db 133 AIGNSLILQNYQLOSPNQOQIPTLISGALR-----MTYGDGVVQQTIV 176
Qy 208 ISGMWLNLSMCVEYVLLWVQYQKTPALAVAGLKEETEELLKOLNLHKDTPXPLEGTHLMG 267
Db 177 TKFVLLAALVGMILTWIIOQYTRGRICRATQDR-----RVVAILG 219
Qy 268 VKDNTNTHEHEQPTCASQMAEPFRTRDGWVSYYNQPVFLAGMGAFLYMTVLFDCI 327
Db 220 INTDVISL-----V 244
Qy 328 TTGYAYTQGLSGSILSILMGASAATGIMGTVAFTWLRRKGGLVRLTGLISGLAQ---- 380
Db 245 TNNYGTDFYIYGFLGIKAFTAVLGGISLDP-----GAMLGGLLLGVAEAQFAGLV 296
Qy 381 -----LSCLLICVSVMP---GSPL 398
Db 297 NSDYKDYFVFSEALLVAVLIFPRPGQLLGRPL 325

RESULT 7
US-09-252-991A-33032
; Sequence 33032, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/1074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33032
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33032

Query Match 3.8%; Score 112; DB 4; Length 305;
Best Local Similarity 18.3%; Pred. No. 0.0063;
Matches 71; Conservative 65; Mismatches 112; Indels 140; Gaps 16;

Qy 48 VFLVLYGNSSLTAVYGLVVAASVVLGAIIQGDWVDKNARLKVAFTSLV---- 97
Db 5 IFLOOMI-NGLTGSGVYGLIAIGYTMVGIIMINFAHGVIMISAYLSAIALALLAFFG 63
Qy 98 VQTVSILGQIILMMVF LHKEHLLTMYHGKVLTSCYLITIANTIANLASTATAI--TI 154
Db 64 LQNPFLLIGLTFLTV----LYTCYGVIER--IAYKPRNSTLAPLISAGMSLI 115
Qy 155 QRDWIVVAGEEDRSKLANNMATTIRIDQLTNLAPMAVGQIMTGSPVIGCGFIS---- 209
Db 116 LQNVQVAQGPORG-----PTLDGAKFH--VGDFVQLTYT K 154
Qy 210 -----GWNLVSMCVBYVLLWKVYQKTPALAVAGLKEETEELKOLNLHKDTEPKPL 260
Db 155 LFILIASLGMVITYVRYTKLGRMCAT-----QODRM----- 190
Qy 261 EGTHIMGVKDSNTHEHEQEPICASQMAEPFRTRDGWVSYNQPFLAGNLAFLYMT 320

RESULT 8

US-09-328-352-4392

Sequence 4392, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton, et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09-0328

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4392

LENGTH: 429

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-4392

Query Match 3.8%; Score 110; DB 4; Length 429;

Best Local Similarity 19.8%; Pred. No. 0.018;

Matches 91; Conservative 78; Mismatches 158; Indels 132; Gaps 23;

Query 20 YILTSAKELLY-LGHS--LSTWGDRMHFAVSFLVELYGNSSLITA---62

Db 4 YIDIIRIIFYNPLSHSYNFNLTMKTKSHQFQSLLYM-LIGSATLIALSIVGRHGFGLYL 62

Query 63 VPMSEHEFGWGHVFSLAJAMONLIWAQOPTGATAADKG----IGDWWDKNRKLKYAQTSLIVVQNVSVILCG 107

Db 63 I-TLMVYFLKHLLTMYHGWLTVSCYLITIANITANLASTATIOTIDWIVVAGED 166

Query 108 16 LCLLMMAF-----SSSVLILNLSLGTLIGLALSATSFVLLSAVRAAPPE 161

Db 116 RSKLANNNATIRRIDQTLNIALPAMYAVQGQIMTGFSPVIGCCFISGWN-----LVSMCV 218

Query 167 RSKLANNNATIRRIDQTLNIALPAMYAVQGQIMTGFSPVIGCCFISGWN-----LVSMCV 218

Db 162 KRSMAMGIAS-----AAGSGCQFMPLPSTLILLTV-CNSSALMVSALLALI 209

Query 219 EYVLLMKVYQKTPALAVKAGLKEETEKLQNLNHKDTPEKP-----LEF 262

Db 210 P--LAWML--KOPSNQTPKAQAPOLTFKOV--LHARKHPPFWNLALGPVFCQQVFLG 264

Query 263 THLMGVKDSNTHELEHQBPCAS----QMAEPPTFRDGVW-SYHNPVFLAGM--312

Db 265 VHLPG-----YLIDGFDAGTGTFLVYGAHVLGDRFSKPKLMALYGS 318

Query 313 -GLAFLYNTVGFDCITGGYY-----TOGLJSGLSILMAGASATG-MGTYAFT 361

Db 319 RGIAIAFLLPPLSTYVV-YAFGIMGLLWSTVLTNGIVANMFGVRYLSMLSGIVF 377

Query 362 WLRRKCGVLVTRGLISGL---AQISCLLICVSYFMPG 395

Db 378 --HQVGSFFGGMLGGVNHDLTGNYNAIWLSIALSILG 413

RESULT 9

US-09-134-001C-4610

Sequence 4610, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm, et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4610
; LENGTH: 470
; TYPE: PRT
; ORGANISM: *Staphylococcus epidermidis*
; US-09-134-001C-4610

Query Match 3.7%; Score 109.5; DB 4; Length 470;

Best Local Similarity 19.5%; Pred. No. 0.023;

Matches 100; Conservative 85; Mismatches 190; Indels 137; Gaps 21;

Qy 73 LVJGAIIGDWD-----KNAKRLKVATSISWVQNVSYVILGQIILMMVFL 115

Db 45 LIGTITFLDAYITITLGTMTDQLTQQPHLSPLATLSIVMTSPLIGALGQGTLAYQFG 104

Qy 116 HXREHLLFMYHGWLTVSCYLITIAN-ANLASTATATIOTDWIVVAGEDR-----167

Db 105 RCR-----ILSLLATLTVTVAAGAAAPVYVILLCRCLMGFAICMDSPVAFTEI 154

Db 105 RCR-----ILSLLATLTVTVAAGAAAPVYVILLCRCLMGFAICMDSPVAFTEI 154

Qy 168 SKLANNNATIRRID--QLTNTLAPAVGQINTFGSPVIGCQ-----FISGWNLVSMCVY 220

Db 155 AEISNLHKGRNUNVYQCVVWVVAITSALVYT-AFPMLGAGAHLMRYAVGFGALIAFYLV 213

Qy 221 VLIWVKYQKTPALAVKAGLKEETEKLQNLNHKDTPEKPLETHMGVKSNDNIELEHEQ 280

Db 214 IIRIKYHESPTWVITHYSLEXATEKIRKYHKD-----THILEGTEDDLN-----259

Db 260 -----SVTSPNSWTDLFKRYTKRILAYAISTIQGMQYYVG-----LVPILA-----306

Qy 281 EPTCASOMAEPPRTFRDGWWSYNNQPVFLA-----GMGLAFLYMTVLGFDCT 328

Db 286 -----SVTSPNSWTDLFKRYTKRILAYAISTIQGMQYYVG-----LVPILA-----306

Qy 329 TGAYATQGLGSLSILMAGASA--ITGIMGTVTAFTWLRKRCGLYRTGLISGLAQSLCIL 386

Db 367 -----TLYLISKDKIGVLTGPAVNAGILGAYLGAQTYLGTRALTMIGFTLVLMSMV 360

Qy 387 CYTSVFMPGSPLDLSSPSFEDIRSPIQGSITP-TKIPBTTIYMNSGNSSANIPET 445

Db 361 CY-GLFLFHPLMLNTF---LIGLFLFGHSGGPFQGXKIGSFPTHLRSQATGFVES 415

Qy 446 SPSVPNTISVSLFAEVIAARIGLMSFLDITVTLQENVIESERGINGVQNSMNYLLDL 505

Db 416 VSRTGSIIGTVPF--PILAAVGLTN-----439

RESULT 10

US-08-118-270-19

Sequence 19, Application US/08118270

Patent No. 5508384

GENERAL INFORMATION:

APPLICANT: Murphy, Randall B.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DC/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118, 270
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/943, 236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34, 033
 REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-197
 TELEX: 202-737-3528
 PCT-US93-08528-19

SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-118-270-19

Query Match Score 108; DB 1; Length 330;
 Best Local Similarity 24.4%; Pred. No. 0.019;
 Matches 51; Conservative 39; Mismatches 71; Indels 48; Gaps 11;

Qy 60 LTAVYGLV---VAGSVILVLAGIIGDWKDNARLKVAQTSLYQNVSVLGIIIMMVF 115
 Db 4 LAAVVGFLLIVTVGNVLVVIAVL----TSRALRAPNLFLVSIASADILVATLMPFS 58

Qy 116 HKHELLTMYHGWLUTSCYLITI---ANIANLASTATAITIQRDWWVVAEDRSKLAN 172
 Db 59 LANEIMWYFGOWCGTylaIDVLFCTSSIVHLC---AISLDRYWSVTOAVE---YN 109

Qy 123 MNATIRRIDLQNTILAPAVGQIMTF----GSPVIGCGF-1SGNNLVSMCVF- 219
 Db 110 LKRPFRVK-ATIVAVLISAVISFPPLVSLYRQPDAAYPQCGLNDETWYILSSCGS 167

Qy 220 -----YVLLW-KVY---QKTPALVK 236
 Db 168 FPAPPCLLIVYARIYVAKRRRTLSK 196

RESULT 11
 PCT-US93-08528-19
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DO/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT-US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/943, 236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34, 033
 REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-197
 TELEX: 246633
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-19

Query Match Score 108; DB 5; Length 330;
 Best Local Similarity 24.4%; Pred. No. 0.019;
 Matches 51; Conservative 39; Mismatches 71; Indels 48; Gaps 11;

Qy 60 LTAVYGLV---VAGSVILVLAGIIGDWKDNARLKVAQTSLYQNVSVLGIIIMMVF 115
 Db 4 LAAVVGFLLIVTVGNVLVVIAVL----TSRALRAPNLFLVSIASADILVATLMPFS 58

Qy 116 HKHELLTMYHGWLUTSCYLITI---ANIANLASTATAITIQRDWWVVAEDRSKLAN 172
 Db 59 LANEIMWYFGOWCGTylaIDVLFCTSSIVHLC---AISLDRYWSVTOAVE---YN 109

Qy 123 MNATIRRIDLQNTILAPAVGQIMTF----GSPVIGCGF-1SGNNLVSMCVF- 219
 Db 110 LKRPFRVK-ATIVAVLISAVISFPPLVSLYRQPDAAYPQCGLNDETWYILSSCGS 167

Qy 220 -----YVLLW-KVY---QKTPALVK 236
 Db 168 FPAPPCLLIVYARIYVAKRRRTLSK 196

RESULT 12
 US-09-489-039A-8237
 Sequence 8237, Application US/09489039A
 ; General Information:
 ; Applicant: Gary Breton et. al.
 ; Title of Invention: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; File Reference: 2709-2004001
 ; Current Application Number: US/09/489, 039A
 ; Patent No. 6610836
 ; Prior Application Number: US 60/117, 747
 ; Prior Filing Date: 2000-01-27
 ; SEQ ID NO: 8237
 ; NUMBER OF SEQ ID NOS: 14342
 ; LENGTH: 549
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-8237

Query Match Score 108; DB 4; Length 549;
 Best Local Similarity 20.5%; Pred. No. 0.042;
 Matches 76; Conservative 51; Mismatches 134; Indels 110; Gaps 13;

Qy 37 WGDRMWHFAVSVFLLVLYGNSLILITAVYGLVAA-TGDNARLKVA-QTS 95
 Db 10 WRQYWPFFGIVIAL----SLLSAANGIGLTAIFI-----NRLITAVDTS 49

Qy 96 LVVQNVSVTLCGIIIMMFLKHETLMYHGMYW-LTSCYLITIANTIANLASTATAIT 153
 Db 50 LRVLPBFLGFLGMLAVTGSQALATTIGHFPRLRREFVRILDQIEQEKGSA-- 107

Qy 154 IQRDWWVVAEDRSKLAMNATIRIDQLTNLAPMAVGQIMTFFSPVIGCGFISG-- 210

108 -----SLLAAGLTSDFIRNITIAFVRPLPEVQGTTILFGSAAY-LAWLSKGM 152
 Db Qy 74 VLGAIIGDWDKNARLKVQTAOTSLLVQNVSVILGIIIMMVFLKHBLTMHGWW- LTSC 132
 211 -----WNLVSMVEYYLWKVYQKTPALAVAKAGLKEEETL----- -KOLNLHHD 254
 Db Qy 170 STGICLTYTGGMKAIVWTD--VFPQVVMVLGF----- -WYLARG 209
 153 LYTTALMAITIWWGFLVLSRKYH----MASLBEETEDKLHYQTIVLEGRKLTLINE 206
 Db Qy 133 YILLITIANILASTATAITIO-----RDNTVVVAG-----
 255 TEPKPBLETHMGVKDSNTHELEHEQPTCAQSMAEPFRDGVSYNQPVFLAGMEL 314
 Db Qy 210 VILGGPENVLSAQHNSRINLMDFDDPRSRYTFTWFLVMSMYGNQAOVQRY 269
 207 RAEYVNQNLQYLPDAREYRHHTVR-----ADTFHLSAVNM---SNIMMLGATOL 251
 Db Qy 165 ----EDRSKLAMMNAIRRIDOLTLNLLAPMAVGQMTFGSPVIGGFSIGL-----
 315 AFLYMFVIGFCITGTYAATGQLSGSILSILMGASAITGIMGTVAFTNLBRKCGLVRTGL 374
 Db Qy 270 VACHTEGRAKLL-----VNOL-----GLFIVASAAAC-CG----- 300
 252 VFWMANSLGW-----ADTAVAATYSLTLL-----FLRTBL 281
 Db Qy 220 YVLLWXYOK--TPALAVKAGLKEEETLQLNLLHDKTEPK-----LEGTH 264
 375 ISGLAQQLSCLI 385
 Db Qy 301 --IVMFYXKDCDPLTRGRISADPONMPLVLDIFEDLPGVGLFLACAYSGTLLSTASTS 358
 282 LSAVGALPTLL 292
 Db Qy 165 ----EDRSKLAMMNAIRRIDOLTLNLLAPMAVGQMTFGSPVIGGFSIGL-----
 359 INAMAATVVEDLIKPRNGGLAR-----KLVFIS-KGLESFIY----GS 396
 Db Qy 265 LMGVKDSNTHELEHEQPTCAQSMAEPFRDGVWSYNNQDVFLAGMGLFLYNTVLGF 324
 376 DCITTGAYTQGSLGSSTISLNGASAITG---IMGTG-----AFT--WLRRKCGL--VR 371
 Db Qy 397 ACITV-----AAUSSLGGVILQGSFTVNGVLSGPLGAFPTGMLPACNTPGVL 446
 325 TGJLSGLAQQLSCLCILCVISVEMPGSPDLVSPPFEDIRSRTFQGESETPTKIPETTEIY 431
 Db Qy 447 SGIAAGLA-VSLWVAATLYPGE-----QTMGVLPSTSAAGCNDNSV 488
 432 M--SNGNSNANIVPETSPE----SVPITSVSLLFAGVTAARIGLWSFDLTVIQL 480
 Db Qy 489 LLGPPGATNANSNGIPSSGMDTGRPALADTVAISLYYGA LG-----TLTML 536
 RESULT 14
 US-08-595-553A-2 ; Sequence 2, Application US/08595553A
 ; Patent No. 6391579
 GENERAL INFORMATION:
 APPLICANT: NANCY CARRASCO, ET AL.
 TITLE OF INVENTION: THYROID SODIUM/IODIDE SYMPORTER AND
 TITLE OF INVENTION: NUCLEIC ACID ENCODING SAME
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: AMSTER, ROTHSCHILD & EBENSTEIN
 STREET: 90 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
 MEDIUM TYPE: DISKETTE
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/595, 553A
 FILING DATE: FEBRUARY 1, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAIG J. ARNOLD
 REGISTRATION NUMBER: 34, 287
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 697-5995
 TELEFAX: (212) 286-0854 or 286-0082
 TELEX: TWX 710-581-4766
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PROTEIN
 DESCRIPTION: RAT
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Rattus sp.
 INDIVIDUAL ISOLATE:
 US-08-595-553A-2 ; Score 108; DB 4; Length 618;
 Query Match 3.7%; Score 108; DB 4; Length 618;
 Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 27;
 Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;
 14 CGSLADYLTSAKFLYLGHSLSWTGDRMMWHPAVSFLVLEYGNSLLITAYGLVYAGSVL 73
 132 CGTLL-QYIVAT--MLYTS-----IVITAPALIINQTVGLDWINSL 169
 14 CGSLADYLTSAKFLYLGHSLSWTGDRMMWHPAVSFLVLEYGNSLLITAYGLVYAGSVL 73
 132 CGTLL-QYIVAT--MLYTS-----IVITAPALIINQTVGLDWINSL 169
 133 YILLITIANILASTATAITIO-----RDNTVVVAG-----
 210 VILGGPENVLSAQHNSRINLMDFDDPRSRYTFTWFLVMSMYGNQAOVQRY 269
 165 ----EDRSKLAMMNAIRRIDOLTLNLLAPMAVGQMTFGSPVIGGFSIGL-----
 Query Match 3.7%; Score 108; DB 4; Length 618;
 Best Local Similarity 19.1%; Pred. No. 0.051; Gaps 27;
 Matches 103; Conservative 71; Mismatches 160; Indels 204; Gaps 27;
 Db Qy 74 VLGAIIGDWDKNARLKVQTAOTSLLVQNVSVILGIIIMMVFLKHBLTMHGWW- LTSC 132
 170 STGICLTYTGGMKAIVWTD--VFPQVVMVLGF----- -WYLARG 209
 Db Qy 133 YILLITIANILASTATAITIO-----RDNTVVVAG-----
 Db Qy 210 VILGGPENVLSAQHNSRINLMDFDDPRSRYTFTWFLVMSMYGNQAOVQRY 269
 Qy 14 CGSLADYLTSAKFLYLGHSLSWTGDRMMWHPAVSFLVLEYGNSLLITAYGLVYAGSVL 73
 132 CGTLL-QYIVAT--MLYTS-----IVITAPALIINQTVGLDWINSL 169

RESULT 15
 US-09-543-681A-8251
 / Sequence 8251, Application US/09543681A
 / Patent No. 6605709
 / GENERAL INFORMATION:
 / APPLICANT: GARY BRETON
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 / FILE REFERENCE: 2709.100-001
 / CURRENT APPLICATION NUMBER: US/09/543, 681A
 / CURRENT FILING DATE: 2000-04-05
 / PRIOR APPLICATION NUMBER: US 60/128, 706
 / PRIOR FILING DATE: 1999-04-09
 / NUMBER OF SEQ ID NOS: 8344
 / SEQ ID NO: 8251
 / TYPE: PRT
 / ORGANISM: Proteus mirabilis
 US-09-543-681A-8251

Query Match 3.7%; Score 107.5; DB 4; Length 491;
 Best Local Similarity 19.7%; Pred. No. 0; Gaps 27;
 Matches 102; Conservative 68; Mismatches 152; Indels 197; Gaps 27;

Qy 29 YLGHSLSTWGDRMWHFA---VSFVELVLYGNS----LLTAVYGLVYAGS--- 71
 Db 28 YLIFSIEMW-ERFGYYGLQG-TMAYLVKMLGNSEAAATTYFAAFTLALVYGFVATCGWLGD 86
 Qy 72 -----VLUVGAATIGDWDKNARLKVAQTSLVQQNVSVLKGII----- 109
 Db 87 KLIIGTKRVITVLGAIV-----LAIGYAMVAFSDDHDKDMIYWGLATIAVGNGLFKANPSS 139
 Qy 110 LMNFVLHRE---LLTMY-----HGWYLTT--SCYLLIITIA 140
 Db 140 LLATCYEKDDPQLDGATFMMYSINVGSFLSMLATPWLAANYGWDVAFAISUVGMILITA 199
 Qy 141 NIANLASTATAITIORDWIVVWAGEDRSKLAMNAT--IRRIDOLTNILAPMAV---- 192
 Db 200 N-----EMLCR6W1-----KDKGSRDPPEPLNYKLULLTGIVALTAVSTWLH 244
 Qy 193 -GQIMTPGSPIVGCGFTSGWNLV-----SMCVEYLLMKVYQKTP 231
 Db 245 NNEVATWLAITLISLGII---LIFARETFMKGVARMIYAFLNVEAVFFVLYDQMP 300
 Qy 232 ALAVKAGIKEETELKOLNLHKDTEPKPLEGTHLMGVKDSNIHELEH----EQEPTCAS 286
 Db 301 T-----SLNFFA-----IHNTVEHALLGFSVBP---- 322
 Qy 287 QMAEPFRFRDGWVSYNNQPVFAGMGLAFLYMTVLGFDCITTGAYTQG--LGSISLSI 344

3.23 ---EQFQSUNPFN----IMLASPLAALY-NFMG-DKLMPYKFTVGMFLSATAFLV 370
 Qy 345 LMGASATTTGIMGTVAFWLRRKGGLVRTG--LIS--GLAQUSCLLCIVS/EMPGLDL 400
 Db 371 LPLGASMANEAGIVSSWLVASYGQS-IGELMISGLAMYAQLVPIRLMGFIMGAWFLT 430
 Qy 401 SVSPFEDIRSRIQESTTPTKIPE----ITTEYMS 433
 Db 431 SAA----AAILAGKVASLIVAPEDVQNAHSLEYSS 463

Search completed: August 17, 2004, 18:08:36
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 18:04:06 ; Search time 50 Seconds

Perfect score: 2929 ; (without alignments)

Sequence: 1 MTRGDHNRQGCCS1ADY.....ACGPDAKEVRKENQANTSVV 571

3585.048 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:^{*}

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4: /cgn2_6/ptodata/1/pubpa/US06_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpa/US10C_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2929	100.0	571	15 US-10-341-434-169	Sequence 169, App
2	2929	100.0	571	15 US-10-341-434-32	Sequence 32, App
3	2925	99.9	571	12 US-10-341-494A-32	Sequence 2, App
4	2924	99.8	571	10 US-09-933-180-2	Sequence 2, App
5	2924	99.8	571	10 US-19-973-180-3	Sequence 3, App
6	2922	99.8	571	10 US-09-933-180-4	Sequence 4, App
7	2917	99.6	571	9 US-09-723-674-130	Sequence 130, App
8	2918	68.9	408	15 US-10-24-861-3007	Sequence 3007, App
9	1789	61.1	382	15 US-10-24-233-1491	Sequence 1491, App
10	1789	61.1	383	10 US-09-899-391-460	Sequence 460, App
11	1789	61.1	383	10 US-09-882-171-460	Sequence 460, App
12	1789	61.1	383	12 US-10-14-861-460	Sequence 460, App
13	656	22.4	484	16 US-10-37-961-157A-54	Sequence 157A-54, App
14	605	20.7	511	16 US-10-425-114-6798	Sequence 6798, App
15	329	11.2	597	12 US-10-425-114-67278	Sequence 67278, App

%

US-10-341-434-169

; ORGANISM: Homo sapiens

US-10-341-434-169

US-10-341-434-169

Query Match Best Local Similarity 100.0% ; Score 2929; DB 15; Length 571;

Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRADHNORGCCSLADYLTSKFLYLGHSLSTWGDRMWHFAVSYFLVELYGNSILL 60

Db 1 MTRADHNORGCCSLADYLTSKFLYLGHSLSTWGDRMWHFAVSYFLVELYGNSILL 60

Qy 61 TAVGIVLWVLTSCYIILITIANILASATATAITQDMIVVAGEDRSKLANNATIRI 120

Db 61 TAVGIVLWVLTSCYIILITIANILASATATAITQDMIVVAGEDRSKLANNATIRI 120

Qy 121 LTMFGWVLTSCYIILITIANILASATATAITQDMIVVAGEDRSKLANNATIRI 180

Db 121 LTMFGWVLTSCYIILITIANILASATATAITQDMIVVAGEDRSKLANNATIRI 180

ALIGNMENTS

```

RESULT 1
; Sequence 169, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
;   APPLICANT: Origene Technologies
;   TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
;   FILE REFERENCE: 9U 204 205 R1
;   CURRENT APPLICATION NUMBER: US/10-341-434
;   CURRENT FILING DATE: 2003-07-18
;   PRIOR APPLICATION NUMBER: US 60/348,164
;   PRIOR FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: US 60/348,119
;   NUMBER OF SEQ ID NOS: 238
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO: 169
;   LENGTH: 571
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-341-434-169
```

Query Match 100.0%; Score 2929; DB 15; Length 571;
 Best Local Similarity 100.0%; Pred No. 1, 7e-272;
 Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRAGDHNRQRGCGSIALADYLSAKFLYLGHSLSTWGDGRMWHFAYSVFLVLYGNSLLL 60
 Db 1 MTRAGDHNRQRGCGSIALADYLSAKFLYLGHSLSTWGDGRMWHFAYSVFLVLYGNSLLL 60

Qy 241 EBBTELKOLNLHKDTERPKPLEGTHLMVGKDSNIHELEHQEOPTCASQMAPFRTRDGWY 300
 Db 241 EBBTELKOLNLHKDTERPKPLEGTHLMVGKDSNIHELEHQEOPTCASQMAPFRTRDGWY 300

Qy 301 SYNQPVLAGMCLAFPLYMTVLGFDCITTGAYTQGLSGSILSILMGASITGIMGTVAP 360
 Db 301 SYNQPVLAGMCLAFPLYMTVLGFDCITTGAYTQGLSGSILSILMGASITGIMGTVAP 360

Qy 361 TWLRKCGLVRGLISQA QNSCLLICVISVMPGSPLDSVSPPEDIRSRFIGESTP 420
 Db 361 TWLRKCGLVRGLISQA QNSCLLICVISVMPGSPLDSVSPPEDIRSRFIGESTP 420

Qy 421 TKIPEITTEYMSNGNSNSANIVPETSPESVPIISVLLFAGVIAARIGMSFDLTVTQI 480
 Db 421 TKIPEITTEYMSNGNSNSANIVPETSPESVPIISVLLFAGVIAARIGMSFDLTVTQI 480

Qy 481 QENVIESERGTINGVQNSMYNLLDLHFIIVTILAPNPEAFGLLVLISVSVFVAMGHIMYFR 540
 Db 481 QENVIESERGTINGVQNSMYNLLDLHFIIVTILAPNPEAFGLLVLISVSVFVAMGHIMYFR 540

Qy 541 FAQNTLNKLFACGPDAKEVRKENQANTSV 571
 Db 541 FAQNTLNKLFACGPDAKEVRKENQANTSV 571

RESULT 2
 US 10-131-496A-32
 Sequence 32, Application US/10331496A
 Publication No. US2003028305A
 GENERAL INFORMATION:
 | APPLICANT: FRANTZ, GRETCHEN J.
 | APPLICANT: HILLIAN, KENNETH J.
 | APPLICANT: PHILLIPS, HEIDI S.
 | APPLICANT: POLAKIS, PAUL
 | APPLICANT: SMITH, VICTORIA
 | APPLICANT: SPENCER, SUSAN D.
 | APPLICANT: WILLIAMS, P. MICKEY
 | APPLICANT: WU, THOMAS D.
 | APPLICANT: ZHANG, JEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF TUMOR

FILE REFERENCE: PS014RL-PCT
 CURRENT APPLICATION NUMBER: US 10/331,496A
 PRIOR APPLICATION NUMBER: US 60/345,444
 PRIOR FILING DATE: 2002-01-02
 PRIOR APPLICATION NUMBER: US 60/351,885
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: US 60/360,056
 PRIOR FILING DATE: 2002-02-25
 PRIOR APPLICATION NUMBER: US 60/362,004
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/366,869
 PRIOR FILING DATE: 2002-03-20
 PRIOR APPLICATION NUMBER: US 60/366,284
 PRIOR FILING DATE: 2002-03-21
 PRIOR APPLICATION NUMBER: US 60/368,679
 PRIOR FILING DATE: 2002-03-28
 PRIOR APPLICATION NUMBER: US 60/404,809
 PRIOR FILING DATE: 2002-08-19
 PRIOR APPLICATION NUMBER: US 60/405,645
 NUMBER OF SEQ ID NOS: 95
 SEQ ID NO: 32
 LENGTH: 571
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: NAME/KEY: misc feature
 LOCATION: (77)-77
 OTHER INFORMATION: The 'Xaa' at location 77 is either Asp or Ala depending on the va

RESULT 3
 US 10/399
 Sequence 2, Application US/10399488
 Publication No. US2004002914A1
 GENERAL INFORMATION:
 | APPLICANT: Pietrangelo, Antonello
 | TITLE OF INVENTION: Mutations in the ferroportin 1 gene associated with hereditary haemochromatosis
 | FILE REFERENCE: 8907-09-939
 | CURRENT APPLICATION NUMBER: US/10/399,488
 | CURRENT FILING DATE: 2003-04-16
 | PRIOR APPLICATION NUMBER: PCT/EP1/12018
 | PRIOR FILING DATE: 2001-10-17
 | PRIOR APPLICATION NUMBER: M12000AA002240
 | PRIOR FILING DATE: 2000-10-17
 | NUMBER OF SEQ ID NOS: 8
 | SOFTWARE: PatentIn version 3.2
 | SEQ ID NO: 2
 | LENGTH: 571
 | TYPE: PRT
 | ORGANISM: Homo sapiens
 | FEATURE: NAME/KEY: misc feature
 | LOCATION: (77)-77
 | OTHER INFORMATION: The 'Xaa' at location 77 is either Asp or Ala depending on the va

Query Match 99.9%; Score 2925; DB 12; Length 571;
 US/10/399,488-2
 Query Match 99.9%; Score 2925; DB 12; Length 571;

Best Local Similarity 99.8%; Pred. No. 4.1e-272; Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTRAGDNRQRGCGSLADYLTSAKELLYGHSLSTWGRMWHFAVSFLVELYGNSSL 60
Db 1 MTRAGDNRQRGCGSLADYLTSAKELLYGHSLSTWGRMWHFAVSFLVELYGNSSL 60

Qy 61 TAVYGLVYAGSVLVLGAIGDWKDNARLKVAQTSLVQNYSVILCGLTMMVFLKHKL 120
Db 61 TAVYGLVYAGSVLVLGAIGDWKDNARLKVAQTSLVQNYSVILCGLTMMVFLKHKL 120

Qy 121 LTMYHGMWLTSCYLITIANLASTATAITIORDWIVVYAGEDRSKLANNNATIRRI 180
Db 121 LTMYHGMWLTSCYLITIANLASTATAITIORDWIVVYAGEDRSKLANNNATIRRI 180

Qy 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGNVLVSCEYLLWKKYQKTPALAVAGLK 240
Db 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGNVLVSCEYLLWKKYQKTPALAVAGLK 240

Qy 241 EETTELKOLNLHKDTDEPKPLETHMGVSKDSNTHELEHQEPCTASOMAEPRTRDGWY 300
Db 241 EETTELKOLNLHKDTDEPKPLETHMGVSKDSNTHELEHQEPCTASOMAEPRTRDGWY 300

Qy 301 SYNNQPVFLAGMGLAFYMTLVGFDCITTGAYTOGJSGLSILSILNGASAATGIMGVAF 360
Db 301 SYNNQPVFLAGMGLAFYMTLVGFDCITTGAYTOGJSGLSILSILNGASAATGIMGVAF 360

Qy 361 TWLRKGCLVRLGLISGLAQLSCLLCLVTSVMPGSPLDLSVPFEDIRSFIGESITP 420
Db 361 TWLRKGCLVRLGLISGLAQLSCLLCLVTSVMPGSPLDLSVPFEDIRSFIGESITP 420

Qy 421 TKPEITIYMSNSANIVPETSPEVPLISLFGVIAARGLWSPLDTVTQLL 480
Db 421 TKPEITIYMSNSANIVPETSPEVPLISLFGVIAARGLWSPLDTVTQLL 480

Qy 481 QENVIESERGLINGVONSNNYLLDLHIMVILAPNEAFGLVLISVSFVAMGHIMYFR 540
Db 481 QENVIESERGLINGVONSNNYLLDLHIMVILAPNEAFGLVLISVSFVAMGHIMYFR 540

RESULT 5
US-09-973-180-3
; Sequence 3, Application US/09973180
; Publication No. US20030082553A1
; GENERAL INFORMATION:
; APPLICANT: Ostra, Ben Heutink, P Duijlin, C.M. Duinin, C.M.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOS FILE REFERENCE: 24584
; CURRENT APPLICATION NUMBER: US/09/973,180
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/301,429
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 144
; OTHER INFORMATION:
; US-09-973-180-3

Query Match 99.8% Score 2924; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 5.2e-272;
Matches 570; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRAGDNRQRGCGSLADYLTSAKELLYGHSLSTWGRMWHFAVSFLVELYGNSSL 60
Db 1 MTRAGDNRQRGCGSLADYLTSAKELLYGHSLSTWGRMWHFAVSFLVELYGNSSL 60

Qy 61 TAVYGLVYAGSVLVLGAIGDWKDNARLKVAQTSLVQNYSVILCGLTMMVFLKHKL 120
Db 61 TAVYGLVYAGSVLVLGAIGDWKDNARLKVAQTSLVQNYSVILCGLTMMVFLKHKL 120

Qy 121 LTMYHGMWLTSCYLITIANLASTATAITIORDWIVVYAGEDRSKLANNNATIRRI 180

RESULT 6
US-09-973-180-4
; Sequence 4, Application US/09973-180
; Publication No. US20030082553A1
; GENERAL INFORMATION:
; APPLICANT: Ostra, Ben Heulinck, P Duijzer, C.M.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FOR AUTOSOMAL DOMINANT HEMOCHROMATOS
; FILE REFERENCE: 24584
; CURRENT APPLICATION NUMBER: US/09/973,180
; PRIOR APPLICATION NUMBER: 60/301,429
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; LOCATION: 144
; OTHER INFORMATION: Xaa = any amino acid except Asp

US-09-973-180-4
Query Match 99.8% Score 2922; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 8e-272;
Matches 570; Conservative 1; Indels 0; Gaps 0;

Qy 1 MTRAGDINRQRGCCGSLADYLTSAKFLYLHSLSLTWGDNRWHPAVSFLVELYGNSSL 60
Db 1 MTRAGDINRQRGCCGSLADYLTSAKFLYLHSLSLTWGDNRWHPAVSFLVELYGNSSL 60
Qy 61 TAVYGLVVAASVYLVGAIIGWDVNARLKVTAQTSLVQVNVSVILCGIIMMVFHKHEL 120
Db 61 TAVYGLVVAASVYLVGAIIGWDVNARLKVTAQTSLVQVNVSVILCGIIMMVFHKHEL 120
Qy 121 LTMYHGVTLSCYLIITIANLASTAATTIORDWIVVAGEDRSKLANNATIRI 180
Db 121 LTMYHGVTLSCYLIITIANLASTAATTIORDWIVVAGEDRSKLANNATIRI 180
Qy 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGMNLVSMCVEYLLNKVYQTKTLA7RAGLK 240

Db 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGMNLVSMCVEYLLNKVYQTKTLA7RAGLK 240
Qy 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGMNLVSMCVEYLLNKVYQTKTLA7RAGLK 240
Db 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGMNLVSMCVEYLLNKVYQTKTLA7RAGLK 240

Db 241 EEBTELKOLNLHKDTKPLETHMGVKDSNTHELEHEOPTCSQMAEPFRFRDGWV 300
Qy 241 EEBTELKOLNLHKDTKPLETHMGVKDSNTHELEHEOPTCSQMAEPFRFRDGWV 300
Db 241 EEBTELKOLNLHKDTKPLETHMGVKDSNTHELEHEOPTCSQMAEPFRFRDGWV 300

Qy 301 SYNQPFLAGNGLAFLYMTVLYGFDCTTGAYTOGLSGLSLISUNGASATGTINGVAF 360
Db 301 SYNQPFLAGNGLAFLYMTVLYGFDCTTGAYTOGLSGLSLISUNGASATGTINGVAF 360
Qy 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360
Db 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360

Qy 361 SYNQPFLAGNGLAFLYMTVLYGFDCTTGAYTOGLSGLSLISUNGASATGTINGVAF 360
Db 361 SYNQPFLAGNGLAFLYMTVLYGFDCTTGAYTOGLSGLSLISUNGASATGTINGVAF 360

Qy 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360
Db 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360

Qy 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360
Db 361 TWLRKCGLVRGLISQAQLSCLLGYATQGLSGLSLISUNGASATGTINGVAF 360

Qy 421 TKPEITTEIYNSGNSANIVPETSPESYPTISVSLFAGVIAARIGLWSFDLTVTQLL 480
Db 421 TKPEITTEIYNSGNSANIVPETSPESYPTISVSLFAGVIAARIGLWSFDLTVTQLL 480
Qy 421 TKPEITTEIYNSGNSANIVPETSPESYPTISVSLFAGVIAARIGLWSFDLTVTQLL 480
Db 421 TKPEITTEIYNSGNSANIVPETSPESYPTISVSLFAGVIAARIGLWSFDLTVTQLL 480

Qy 481 QENVIESERGLINGVQNSMNYLDDLFIMVILAPNEAFGLVVLISVSTVAGHIMYFR 540
Db 481 QENVIESERGLINGVQNSMNYLDDLFIMVILAPNEAFGLVVLISVSTVAGHIMYFR 540
Qy 541 FAQNTLGNRLFACGPDAKEVKENQANTSVV 571
Db 541 FAQNTLGNRLFACGPDAKEVKENQANTSVV 571
Qy 541 FAQNTLGNRLFACGPDAKEVKENQANTSVV 571
Db 541 FAQNTLGNRLFACGPDAKEVKENQANTSVV 571

RESULT 7
US-09-729-574-130
; Sequence 130, Application US/09729674
; Patent No. US2001039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cherry
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostoni, Michael J.
; APPLICANT: Steininger, II, Robert J.
; APPLICANT: Spaulding, Vicki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Pechtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 6055-6A
; CURRENT APPLICATION NUMBER: US/09/729,674
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF EQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 130
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: ; UNSURE
; LOCATION: (202)
; NAME/KEY: ; UNSURE
; LOCATION: (504)
; US-09-729-574-130
Query Match 99.6% Score 2917; DB 9; Length 571;
Best Local Similarity 99.6%; Pred. No. 2.4e-271;
Matches 569; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MTRAGDINRQRGCCGSLADYLTSAKFLYLHSLSLTWGDNRWHPAVSFLVELYGNSSL 60
Db 1 MTRAGDINRQRGCCGSLADYLTSAKFLYLHSLSLTWGDNRWHPAVSFLVELYGNSSL 60
Qy 61 TAVYGLVVAASVYLVGAIIGWDVNARLKVTAQTSLVQVNVSVILCGIIMMVFHKHEL 120
Db 61 TAVYGLVVAASVYLVGAIIGWDVNARLKVTAQTSLVQVNVSVILCGIIMMVFHKHEL 120
Qy 121 LTMYHGVTLSCYLIITIANLASTAATTIORDWIVVAGEDRSKLANNATIRI 180
Db 121 LTMYHGVTLSCYLIITIANLASTAATTIORDWIVVAGEDRSKLANNATIRI 180
Qy 181 DQLTNILAPMAVGQIMTGFSPVIGCFISGMNLVSMCVEYLLNKVYQTKTLA7RAGLK 240

Qy 61 TAVYGLVYAGSVIYLGAIGDWDKNARLKVQATSILVQNVSVILGVIIIMVFLKHKL 120
 Db 61 TAVYGLVYAGSVIYLGAIGDWDKNARLKVQATSILVQNVSVILGVIIIMVFLKHKL 120
 Qy 121 LTMYHGNWLTSCXILITIANLIASTATAATTIQRDWIVVAGEDRSKLANMNTIRI 180
 Db 121 LTMYHGNWLTSCXILITIANLIASTATAATTIQRDWIVVAGEDRSKLANMNTIRI 180
 Qy 161 DQITNLMPMANGQIMTGFSPVIGCPIGSIGNLVSNCEYVLLWKKYQKTPALAKGLK 240
 Db 161 DQITNLMPMANGQIMTGFSPVIGCPIGSIGNLVSNCEYVLLWKKYQKTPALAKGLK 240
 Qy 241 EEBTELKOLNLHKDTPEPLEGTHLMGVDSNIELEHQEPCTASQMAEPFRFRDGWV 300
 Db 241 EEBTELKOLNLHKDTPEPLEGTHLMGVDSNIELEHQEPCTASQMAEPFRFRDGWV 300
 Qy 301 SYNNQPVLFLAGLAFYMTLVGFDCITGTAYTOGSGSLSLUNGASAATGIMGTVAF 360
 Db 301 SYNNQPVLFLAGLAFYMTLVGFDCITGTAYTOGSGSLSLUNGASAATGIMGTVAF 360
 Qy 361 TWLRKCGCLVRLGLISGIAQLSCLLICVSYMPGSPFLDSVSPFDIRSFQGESITP 420
 Db 361 TWLRKCGCLVRLGLISGIAQLSCLLICVSYMPGSPFLDSVSPFDIRSFQGESITP 420
 Qy 421 TKPEITTEIYMSNGNSSANIVPETSPESSVPLISLFAVGTAARIGLINSFDLTQIL 480
 Db 421 TKPEITTEIYMSNGNSSANIVPETSPESSVPLISLFAVGTAARIGLWSFDLTQIL 480
 Qy 481 QENVIESERGLINGVNQSMNYLLDIFLIMTILAPNEAFGLLVLISVSFTAMGHIMYR 540
 Db 481 QENVIESERGLINGVNQSMNYLLDIFLIMTILAPNEAFGLLVLISVSFTAMGHIMYR 540
 Qy 541 FAQNTLGNKLFACPDAKEVRKENQANTSVV 571
 Db 541 FAQNTLGNKLFACPDAKEVRKENQANTSVV 571

RESULT 8
 US-10-264-049-3007
 ; Sequence 3007, Application US/10264049
 ; GENERAL INFORMATION: Publication No. US200400557341
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; PRIORITY APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIORITY NUMBER: US 60/205, 515
 ; PRIORITY FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NO: 28/6
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO: 1491
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-264-237-1491
 Query Match 61.1%; Score 1789; DB 15; Length 382;
 Best Local Similarity 92.4%; Pred. No. 4.e-16;
 Matches 355; Conservative 3; Mismatches 26; Indels 0; Gaps 0;
 File Reference: PA131P1
 Current Application Number: US/10/264,237
 Current Filing Date: 2002-10-04
 Prior Application Number: PCT/US01/16450
 Prior Filing Date: 2001-05-18
 Prior Application Number: US 60/205, 515
 Prior Filing Date: 2000-05-19
 Number of Seq Id No: 28/6
 Software: PatentIn Ver. 3.1
 Seq Id No: 3007
 Length: 408
 Type: PRT
 Organism: Homo sapiens

US-10-264-049-3007
 Query Match 68.9%; Score 2018; DB 15; Length 408;
 Best Local Similarity 100.0%; Pred. No. 4. 6.e-18;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 RIDOLNTIAPMAYGQIMTFGSPIVGCFISGWNLYSMCVEYLWKKYQKTPALAKAG 238
 Db 16 RIDOLNTIAPMAGQIMTFGSPIVGCFISGWNLYSMCVEYLWKKYQKTPALAKAG 75
 Qy 239 LKEEETELKOLNLHKDTPEPLEGTHLMGVDSNIELEHQEPCTASQMAEPFRFRDG 298
 Db 76 LKEEETELKOLNLHKDTPEPLEGTHMGVDSNIELEHQEPCTASQMAEPFRFRDG 135
 Qy 299 WWSYNNQPVLFLAGLAFYMTLVGFDCITGTAYTOGSGSLSLUNGASAATGIMGTV 358
 Db 361 LFACCPDAKEVRKENQANTSVV 571
 Qy 376 FRFAQNTLGNKLFACPDAKEVRKENQANTSVV 408

RESULT 9
 US-10-264-237-1491
 ; Sequence 1491, Application US/10264237
 ; Publication No. US2004005491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIORITY NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIORITY NUMBER: US 60/205, 515
 ; PRIORITY FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NO: 28/6
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO: 1491
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-264-237-1491
 Query Match 61.1%; Score 1789; DB 15; Length 382;
 Best Local Similarity 92.4%; Pred. No. 4.e-16;
 Matches 355; Conservative 3; Mismatches 26; Indels 0; Gaps 0;
 File Reference: PA131P1
 Current Application Number: US/10/264,237
 Current Filing Date: 2002-10-04
 Prior Application Number: PCT/US01/16450
 Prior Filing Date: 2001-05-18
 Prior Application Number: US 60/205, 515
 Prior Filing Date: 2000-05-19
 Number of Seq Id No: 28/6
 Software: PatentIn Ver. 3.1
 Seq Id No: 3007
 Length: 408
 Type: PRT
 Organism: Homo sapiens

US-10-264-049-3007
 Query Match 68.9%; Score 2018; DB 15; Length 408;
 Best Local Similarity 100.0%; Pred. No. 4. 6.e-18;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 RIDOLNTIAPMAYGQIMTFGSPIVGCFISGWNLYSMCVEYLWKKYQKTPALAKAG 238
 Db 16 RIDOLNTIAPMAGQIMTFGSPIVGCFISGWNLYSMCVEYLWKKYQKTPALAKAG 75
 Qy 239 LKEEETELKOLNLHKDTPEPLEGTHLMGVDSNIELEHQEPCTASQMAEPFRFRDG 298
 Db 76 LKEEETELKOLNLHKDTPEPLEGTHMGVDSNIELEHQEPCTASQMAEPFRFRDG 135
 Qy 299 WWSYNNQPVLFLAGLAFYMTLVGFDCITGTAYTOGSGSLSLUNGASAATGIMGTV 358
 Db 361 LFACCPDAKEVRKENQANTSVV 382

RESULT 10
 US-09-809-391-460 ; Sequence 460, Application US/09809391
 ; Publication No. US20030049618A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT FILING DATE: 2001-03-16
 ; Prior application data removed - consult PALM or file wrapper
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 460
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: SITE
 ; NAME/KEY: SITE
 ; LOCATION: (383)
 ; OTHER INFORMATION: Xaa equals stop translation
 US-09-809-391-460

Query Match 61.1% Score 1789; DB 10; Length 383;
 Best Local Similarity 92.4%; Pred. No. 4..6e-163; Indels 0; Gaps 0;
 Matches 353; Conservative 3; Mismatches 26;

Qy	190	MAVGQIMTFGPSPVIGCPFISGNLVSMDVYQKTPALAVKAGIKEEETELKQI
D _b	1	MAVGQIMTFGPSPVIGCFISGNLVSMDVYQKTPALAVKAGIKEEETELKQI
Qy	250	NLHKDTFPKPLETHLMGVKDSNTHELEBQEPCTASQMAEPFRDGVSYNNQPVFL
D _b	5	NLHKDTFPKPLETHLMGVKDSNTHELEBQEPCTASQMAEPFRDGVSYNNQPVFL
Qy	310	AGMGLAFLYMTVLGFDCITGYAYTOQLSGSILSILMGASAATGIMGTVFTWLRKCGI
D _b	121	AGMGLAFLYMTVLGFDCITGYAYTOQLSGSILSILMGASAATGIMGTVFTWLRKCGI
Qy	370	VRTGLISGLAQLSCLILCVISVMPGSPLDVSPEIDTSRFQEGESTPTKIPETIE
D _b	181	GSAGLISGLAQLSCLILCVISVMPGSPLDVSPEIDTSRFQEGESTPTKIPETIE
Qy	430	IMSGNSNSANIVPETSPEVSPVIIISLLPAGVIAARIGHWSFDLTQLOQEVIESER
D _b	241	IMSGNSNSANIVPETSPEVSPVIIISLLPAGVIAARIGHWSFDLTQLOQEVIESER
Qy	490	GLINGVNSNSNYLLDLHFMVILANPFAGLLVLISSEVAMHIMYFRFAQNTLGNK
D _b	301	GLINGVNSNSNYLLDLHFMVILANPFAGLLVLISSEVAMHIMYFRFAQNTLGNK
Qy	550	LFACGPDAKEVRKENQANTSVV
D _b	361	LFACGPDAKEVRKENQANTSVV

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 ; PRIOR APPLICATION NUMBER: 60/0040,162
 ; PRIOR FILING DATE: 1997-03-07
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 ; PRIOR APPLICATION NUMBER: 60/0038,621
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RESULT 11
 US-09-882-171-460 ; Sequence 460, Application US/09882171
 ; Publication No. US20030175859A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 09/809,391
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 09/149,476
 ; PRIOR FILING DATE: 1998-09-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493

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 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/057,669
 PRIOR FILING DATE: 1997-09-05

Query Match 61.1%; Score 1789; DB 10; Length 383;
 Best Local Similarity 92.4%; Pred. No. 4; Gaps 0;
 Matches 353; Conservative 3; Mismatches 26;
 Indels 0; Gaps 0;

Qy 190 MAVGQIMTGSPTVIGGFISGNLVSMSMCYEVILWKKYQKTPALAKAGLKEETELKQL 249
 Db 1 MAVGQIMTGSPTVIGGFISGNLVSMSMCYEVILWKKYQKTPALAKAGLKEETELKQL 60

Qy 250 NLHKDTEPKPLEGTHLMGVKDSDNTHEEQEPTCAGSMAEPRTFRDGWTSYYNPVFL 309
 Db 61 NLHKDTEPKPLEGTHLMGVKDSDNTHEEQEPTCAGSMAEPRTFRDGWTSYYNPVFL 120

Qy 310 AGMGAFLMTVQLSCILCVTSVMPGSPDLSTSPTFEDRSRPTQGESETPTKIPETTE 369
 Db 121 AGMGAFLMTVQLSCILCVTSVMPGSPDLSTSPTFEDRSRPTQGESETPTKIPETTE 180

Qy 370 VRTGLISGLAQSLCILCVTSVMPGSPDLSTSPTFEDRSRPTQGESETPTKIPETTE 429
 Db 181 GSAGGIGAQLSCILCVTSVMPGSPDLSTSPTFEDRSRPTQGESETPTKIPETTE 240

Qy 430 IYMSNGNSSANIVPETSPTSPSVPLISSLIFAGVIAARGLWSPLDTTQLQENVIESER 489
 Db 241 IYMSNGNSSANIVPETSPTSPSVPLISSLIFAGVIAARGLWSPLDTTQLQENVIESER 300

Qy 490 GTINGQNSNYLDDLHIMVILAPNEAFGLLISYSFAMGHIMYFRAQNTLGNK 549
 Db 301 GTINGQNSNYLDDLHIMVILAPNEAFGLLISYSFAMGHIMYFRAQNTLGNK 360

Qy 550 LFACCPDAEVRKRNQANTSVV 571
 Db 361 LFACCPDAEVRKRNQANTSVV 382

RESULT 12

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; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 157454
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57023C.1.pep
; US-10-437-963-157454

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Query Match 22.4%; Score 556; DB 16; Length 484;

	Best Local Similarity	Score	Pred.	No.	Indels	Gaps
Matches	29.9%	556	6.8e-54	91	Mismatches	169
Db	27	LYTGHFSLRGARMWESVGLYMRIWPGSLLTAVYGVVEASAYAALGPVGVAVDRLA 86				
Qy	28	LYTGHFSLTGDMWHFAVSFLVELVGNSSLTAVYGVVAGSVLVLGAIIGDWYDNA 87				
Qy	88	RKVAQTSLVVONVSVILCGIILMMYFLRKHLLTYHGHWLTSCLYLITIANI---A 143				
Db	87	YLOVRLRMLLQGASFYAAG/SVTALVYGAHLAA-GF--PAFVALVVTNVSGALA 141				
Qy	144	NLASTADAITIORDWIVVVA-GEDRSKLANNATIRRIDLNTIAPMAYQOIMTFGSPV 202				
Db	142	AUSTLAGTILBREWWVIAQGQPAAVLGINSVIRIDUSCKLIALPVLSQFFISVSME 201				
Qy	203	IGGGFISGWNLVSMCMVYVLLWKKYQKTPALAVAKGLKEETELKQLNLHKDTEPKPLEG 262				
Db	202	ASAALAWNLAAWWVYWPVSVTAAGPFA-----SETSOISRERADDDE---- 247				
Qy	263	THLMGVDSNTHELEHEQEPICASQNAEPEPTFR-----DGWSYYNNQPVFLAGMG 313				
Db	248	-----AAAQQPKVERLWMTLPCWESWAVARQEYVLPGVIA 285				
Qy	314	LAFLYMMVLFQDCITTYQAYTQGLSSSILSILMGASAITGMGTVAFTWLRRKCOLVRTG 373				
Db	286	LAFLYFLVLFQDTLMVATLDNEGIAPVVISLARGVSAAVGAATWVPAAHARYSTLRAG 345				
Qy	374	LISGLAOLSCLLICVISVMPGSPLDLSVSPFEDIRSRTQGESTITKPEITIBYMS 433				
Db	346	LNSIWAQMCCLVCVASSWAGG----- 367				
Qy	434	NGNSNSANIVPETSPEPSVPIISLIPAGVIAARIGWSFDLTIVTOLQENVIESERIIN 493				
Db	368	-----APLASAMWLGVVAASRLGWMFDIAVMQLMQDGVPESDRCVVG 412				

SEQ ID NO: 67781
 LENGTH: 511
 TYPE: PRT
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3632-036-H10_FLI.pep
 US-10-425-114-67781

Query Match 20.7%; Score 605; DB 12; Length 511;
 Best Local Similarity 28.2%; Pred. No. 5.9e-19;
 Matches 152; Conservative 103; Mismatches 186; Indels 98; Gaps 10;

Qy 13 CCGSLADWLTSAKFL--LYLGHSLSTWGDRWHFAVSFLVELYGNSSLTAVYGLVAGSVLVLGAIIGWVDK 85
 Db 40 CGSS--PILDAPILRYYAGQILARQARYMIRIWPSLFLFATIYGVETS 96

Qy 71 SVLVLGATIAGDWDYDKNARLKVAQTSLTVQNVSLCILMMVFLKHLLTMHGWLTL 130
 Db 97 SLVVLGPVGTLYGRATYQLVGLWILQSILIVAGTSVITLMLYANLRLATSF----- 150

Qy 131 SCYLITITANI---ANALASTATAATTIORDWIVV-AGEDRSKLANMNATIRRIDOLTN 185
 Db 151 PAFNALVAVTNVSGALLAALSAGTLLIEREAVVVVSSGHPPSVRTGINSVRRDLGCS 210

Qy 186 ILAPMAYGOINTMFGSPVTCGFPISGMNIVSMCMEVYLLMKVYQKTPALAKAGLKEETE 245
 Db 211 LIAPIVLSVIALSTQASAVALSTAASAGIQCYCLFVSYNGVPAIAAPROPRASDAE 270

Qy 246 LKQNLNHLKDTPEKPLETHMGVYKDSNINHELEHQPTCA---SOMAEPRTFR--DGW 299
 Db 271 -----RPPPVPMT-----VAFAEAETQALDWRAALDKLSVASGWESEW 309

Qy 300 VSYYNQPVPLLAGNGLAFFYMTVLFQDCLITGAYTQSGSILSINGASATIGMTVA 359
 Db 310 VIYARQDVLPVGAVALAFTYFTULSFGTLMATATLDWKGIPAVTISARGFAIVGIGATLL 369

Qy 360 FTWLRRKCGVRGLISCLGLAQSLCLTIVISVMPGSPLDSVSPPEDIRSRIFIGESTIT 419
 Db 370 YPLVHSRVSTLRTGLWISWMQCCLLIVASVW----- 402

Qy 420 PTKIPETTEIYMSNGNSANIVPTEPESPYIISVSLFQVIAARIQWSFDLTVYQL 479
 Db 403 -----AAATVAVSAMWLMQGVAASRGLWTFDAMQL 434

Qy 480 LQENVIESBERGLINGQNSNMYLDDIFINVILAPNPEAGLVLIVSFSVANGHIMY 538
 Db 435 MQDGVDPDIERCVSGVQNALQSVDLITYVAVISDPKDFSKMIVLSSLVTCAAVMY 493

Query Match 11.2%; Score 329; DB 12; Length 597;
 Best Local Similarity 22.9%; Prod. No. 2.7e-22;
 Matches 125; Conservative 220; Mismatches 220; Indels 114; Gaps 14;

Qy 26 FLYLGHSLSTWGDRWHFAVSFLVELYGNSSLTAVYGLVAGSVLVLGAIIGWVDK 85
 Db 145 YALYASVLFQNLVEQLNRFPAWTALIHPN-LVPAVLFGFPTKLSFVGAPIVGKLMHD 203

Qy 86 NARUJVAOTSLWQ-INVSLCILMMVFLKHLLTMHGWLTL 144
 Db 204 FPRPMTALNAVQGTQQLISARTIVYALRNLSHASTTAV--VLRPWFIALVAGALER 260

Qy 145 LASTATAATTIORDWIVVAGEDRS-KLANMNATIRRIDOLTNLAPMAVGQIMTFSGPVI 203
 Db 261 LAGALGSMERDVNVVLAGTRNPVALQANAUNRLDVLVCTVGAJVGLLSSKHFPT 320

Qy 204 GCGFISGMNLVSMCMEVYLLWKVYQKTPALAKAGLKEETELKQNLNHLKDTEPKPLEGT 263

Db 321 CLKIASGMNICS-----PVLYM-----LGQI----- 342

Qy 264 HLMVYKDSNINHELEHQ---EPTCASOM-----AEPPERTFRDGWVSYNNOPVFLAGMG 313
 Db 343 -----INRYVSCHALDSRTATDESICADDLVRVPIVNSLRA-KHGNNEYKQQTVPASSA 398

Qy 314 LAFLMMTV-LGFDGTTGAYTQGSGSISLIMGASAATG-MGTWAPTWLRKCGLVRT 372
 Db 399 TVEFLNENTALAPGBMTTALMHRGTSPTVNGAFLSGSLSIMGIVATISSUVKRGVLKA 458

Qy 373 GLISGSQLSCLTLCIVSMPGSPLDLSVSPPEDIRSRIFIGESTITPKIPEITIBYM 432

Db 459 G-AGLIFOAISLISIALITYWAS----- 481

Qy 433 SNGSNANTVPEPSPESPYIISVSLFLGAVIAARIQWSFDLTVTOLQENVIESSERGII 492
 Db 482 -----ISQTPLJLFLASAL-----SRLGHSYDVGTQVGTYPASXANLI 525

Qy 493 NGVQNSMNYYLDLIDIFINVILAPNPEAGLVLIVSFSVANGHIMYFRAQNTLG--NKL 550
 Db 526 GMEVSIASIAEYLMLANAAIANDVSHGFLAIISSVAGAWMFCRWLNTNPTEOREL 585

Qy 551 FACSP 555
 Db 586 FMVDP 590

Search completed: August 17, 2004, 18:10:18
 Job time : 52 secs

RESULT 15

US-10-425-114-67278

Sequence 67278, Application US/10425114

GENERAL INFORMATION

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Soreen, Steven E.

APPLICANT: Tabaski, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10425114

SEQUENCE ID NO: 67278

LENGTH: 597

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: LIB4759-026-A6_FLI.pep

US-10-425-114-67278

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Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6
CM protein - protein search, using sw model	
Run on:	August 17, 2004, 17:56:35 ; Search time 43 Seconds (without alignments)
Title:	US-09-715-927-6
Perfect score:	29.9
Sequence:	1 MTRAGDHNRRQRGCGSLADY.....ACGDDAKEVRKENQANTSVV 571
Scoring table:	BLOSUM62
Gapop 10.0 , Gapext 0.5	
Searched:	1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters:	1017041
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Database :	SPTREMBL 25:*
	1: sp_archaea:*
	2: sp_bacteria:*
	3: sp_fungi:*
	4: sp_human:*
	5: sp_invertebrate:*
	6: sp_mammal:*
	7: sp_mhc:*
	8: sp_organelle:*
	9: sp_phage:*
	10: sp_plant:*
	11: sp Rodent:*
	12: sp_virus:*
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	14: sp_unclassified:*
	15: sp_rvirus:*
	16: sp_bacteriophage:*
	17: sp_archeap:*
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	AC Q9NP59; PRT; 571 AA.
	DT 01-OCT-2000 (TREMBIrel. 15, Created)
	DT 01-OCT-2000 (TREMBIrel. 15, Last sequence update)
	DT 01-OCT-2003 (TREMBIrel. 25, Last annotation update)
	DE Iron-regulated transporter IREG1 (Ferroportin) (Hypothetical protein)
	DE (Solute carrier family 11 (Proton-coupled divalent metal ion transporters) member 3).
	GN IREG1 OR FPN1 OR DKFP586J0624.
	OS Homo sapiens (Human).
	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	OX NCBI_TaxID=9606;
	RN [1]
	SEQUENCE FROM N.A.
	RX MEDLINE=0337919; PubMed=10882071;
	RA McKee A.T., Marciani P., Rolfs A., Brennan K., Wehr K., Barrow D.,
	RA Mirset T., Bonfورد A., Peters T.J., Farzaneh F., Hediger M.A.,
	RA Hentze M.W., Simpson R.J.;
	RT "A novel duodenal iron-regulated transporter, IREG1, implicated in the basolateral transfer of iron to the circulation." Mol. Cell 5:29-39(2000).
	RL [2]
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	RC TISSUE=Placenta;
	RC MEDLINE=0115574; PubMed=10693807;
	RA Donovan A., Brownlie A., Zhou Y., Shepard J., Pratt S.J., Moynihan J.,
	RA Paw B.H., Drrijer A., Barut B., Zapata A., Law T.C., Brunner C.,
	RA Lux S.B., IV, Pinkus G.S., Kingsley P.D., Palis J.,
	RA Fleming M.D., Andrews N.C., Zon L.I.;
	RT "Positional Cloning of Zebrafish Ferroportin Identifies a Conserved Vertebrate Iron Exporter." RT Nature 403:776-781(2000).
	RL [3]
	RN SEQUENCE FROM N.A.
	RC TISSUE=Uterus;
	RA Duesterhoeft A., Lauber J., Newes H.W., Gassenhuber J., Wiemann S.;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	299.9	100.0	571	4	Q9NP59	Q9np59 homo sapien
2	292.1	99.7	571	4	Q8IVB2	Q8ivb2 homo sapien
3	290.6	99.2	571	4	Q9NPB2	Q9nrb2 homo sapien
4	261.8	89.4	570	11	Q9ATH19	Q9ath19 mus musculus
5	261.5	89.2	570	11	Q9AKP4	Q9akp4 mus musculus
6	260.5	88.8	570	11	Q923U9	Q923u9 rattus norvegicus
7	1975.5	67.4	562	13	Q8IFW0	Q8ifw0 brachydanio rerio
8	1971.5	67.3	562	13	Q919R3	Q919r3 brachydanio rerio
9	1894.5	64.7	528	13	Q8AW23	Q8aw23 brachydanio rerio
10	1519.5	51.7	436	13	Q8AW28	Q8aw28 brachydanio rerio
11	1479.5	50.5	405	11	Q921C9	Q921c9 zattus norvegicus
12	1360.5	46.4	305	11	Q8BMES	Q8bmes mus musculus
13	1021.5	34.9	310	13	Q7Z251	Q7zz251 brachydanio rerio
14	859	29.3	167	4	Q9NTS1	Q9nts1 homo sapien
15	677	23.1	133	4	Q7ZF8	Q7zf8 homo sapien
16	612.5	20.9	524	10	Q88905	Q88905 arabidopsis

RL Submitted (JAN-2000) to the EMBL/GenBank/NCBI databases.

RN [4] Sequence from N.A.

RC TISSUE-Testis;

RA Submitted (SEP-2002) to the EMBL/GenBank/NCBI databases.

RL Submitted (SEP-2002) to the EMBL/GenBank/NCBI databases.

EMBL; AF231121; AAF44330.1; -.

DR EMBL; AF226614; AAF36597.1; -.

DR EMBL; AL136914; CAB66578.1; -.

DR EMBL; BC037733; AAH37733.1; -.

DR Gene; HGNC:SLC40A1; -.

DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.

DR GO; GO:0005488; F:binding; IEA.

DR GO; GO:0006110; P:transport; IEA.

DR InterPro; IPR001993; Mitoch carrier.

DR PROSITE; PS00215; MITOCH_CARRIER; 1.

KW Hypothetical protein in:

SEQUENCE 571 AA; 62542 MW; E4D655949C904959 CRC64;

SEQUENCE 100.0%; Score 2929; DB 4; Length 571;

Best Local Similarity 100.0%; Pred. No. 8.7e-220; Gaps 0;

Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTAGDNRQRGCGSIALDYTSKAKFLYLGHSLSTWGDRMWHFAYSVFLYLYGNSSL 60

Db 1 MTAGDNRQRGCGSIALDYTSKAKFLYLGHSLSTWGDRMWHFAYSVFLYLYGNSSL 60

Qy 61 TAVYGLVAGSVLVGLATTGDAVDKNARLRYAQTSLVQNVSVILCGIILMMVFHLKHEL 120

Db 61 TAVYGLVAGSVLVGLATTGDAVDKNARLRYAQTSLVQNVSVILCGIILMMVFHLKHEL 120

Qy 121 LTMYHGAVLTSCYLIITIANLASTATAATTIORDWIVVVAGEDRSKLANNATIRR 180

Db 121 LTMYHGAVLTSCYLIITIANLASTATAATTIORDWIVVVAGEDRSKLANNATIRR 180

Qy 121 LTMYHGAVLTSCYLIITIANLASTATAATTIORDWIVVVAGEDRSKLANNATIRR 180

Db 121 LTMYHGAVLTSCYLIITIANLASTATAATTIORDWIVVVAGEDRSKLANNATIRR 180

Qy 181 DQTNILAPMAVGQIMTGFSPVIGCGTISGNLVSNCVEYLLWKVYQKTPALAVAGLK 240

Db 181 DQTNILAPMAVGQIMTGFSPVIGCGTISGNLVSNCVEYLLWKVYQKTPALAVAGLK 240

Qy 181 DQTNILAPMAVGQIMTGFSPVIGCGTISGNLVSNCVEYLLWKVYQKTPALAVAGLK 240

Db 181 DQTNILAPMAVGQIMTGFSPVIGCGTISGNLVSNCVEYLLWKVYQKTPALAVAGLK 240

Qy 241 EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHEPHEQPTCASOMABPFTRFRGMY 300

Db 241 EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHEPHEQPTCASOMABPFTRFRGMY 300

Qy 301 SYNQPLAGMGLAFLYMTWVGLFDCITTGAYTQGIGSLSLISLGMASAITGNGTVAF 360

Db 301 SYNQPLAGMGLAFLYMTWVGLFDCITTGAYTQGIGSLSLISLGMASAITGNGTVAF 360

Qy 361 TWLRKCCVLVRTLGLSGLAQSLCLLICVISVMPGSPLDLVSPFEDIRSRFIQGESITP 420

Db 361 TWLRKCCVLVRTLGLSGLAQSLCLLICVISVMPGSPLDLVSPFEDIRSRFIQGESITP 420

Qy 361 TWLRKCCVLVRTLGLSGLAQSLCLLICVISVMPGSPLDLVSPFEDIRSRFIQGESITP 420

Db 421 TKPEITTEIYNSGNSANIVPETSPEVPLISVSLFLAGVIAARIGLMSFDLTVTQLL 480

Qy 421 TKPEITTEIYNSGNSANIVPETSPEVPLISVSLFLAGVIAARIGLMSFDLTVTQLL 480

Db 421 TKPEITTEIYNSGNSANIVPETSPEVPLISVSLFLAGVIAARIGLMSFDLTVTQLL 480

Qy 481 QENVIESRGINGVQNSMNYLDDLFIMVILAPNEAFGLLVLVLSVSFVAMGHIMYFR 540

Db 481 QENVIESRGINGVQNSMNYLDDLFIMVILAPNEAFGLLVLVLSVSFVAMGHIMYFR 540

Qy 541 FAQNTLGNKLPGCPDAKEVRKENQANTSVV 571

Db 541 FAQNTLGNKLPGCPDAKEVRKENQANTSVV 571

Qy 541 FAQNTLGNKLPGCPDAKEVRKENQANTSVV 571

Db 541 FAQNTLGNKLPGCPDAKEVRKENQANTSVV 571

RESULT 3

Q9NRL0 PRELIMINARY; PRT; 571 AA.

AC Q9NRL0; PRELIMINARY; PRT; 571 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE S1-C1A3 iron transporter.

OS Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

DE transporters), member 3.

RESULT 2

Q8IVB2 PRELIMINARY; PRT; 571 AA.

ID Q8IVB2; PRELIMINARY; PRT; 571 AA.

AC Q8IVB2; PRELIMINARY; PRT; 571 AA.

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-OCT-2003 (TREMBLrel. 23, Last sequence update)

DE Solute carrier family 11 (Proton-coupled divalent metal ion

DE transporters), member 3.

OX	NCBI_TAXID=9606;	PRT; 570 AA.
RN	[1] SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A., PubMed=10747949;	
PK	PMID:20347902, PubMed=10747949;	
RA	"Assignment of slc11a3 to mouse chromosome 1 band 1B and SLC11A3 to human chromosome 2q32 by <i>in situ</i> hybridization.";	
RR	Human Mammalian Iron-regulated Protein Involved in Intracellular Cytochrome C Integgral to plasma membrane; TAS.	
RL	Cell. Genet. 88:328-329(2000).	
DR	GO:0005777; C:cytoplasm; TAS.	
DR	GO:0005887; C:integral to plasma membrane; TAS.	
DR	GO:0007345; P:embryogenesis and morphogenesis; TAS.	
DR	GO:0006819; P:iron ion homeostasis; TAS.	
DR	GO:0006846; P:iron ion transport; TAS.	
DR	InterPro: IPD001933; Mitoch carrier.	
DR	PS00215; MitoCH CARRIER; 1.	
SQ	SEQUENCE 571 AA; 62581 MW; 8870/BFFC4A4B921 CRC64;	
Query Match	Score 99.2%; Best Local Similarity 99.5%; Matches 568; Conservative 0; Mismatches 0; Indels 3; Gaps 0;	Length 571;
DB	1 MTAGDNHQRCGCGSLADYLTSAKFLYLGHLSLSTWGRMWHFAYSVFLVLYGNSSL 60	
DB	1 MTAGDNHQRCGCGSLADYLTSAKFLYLGHLSLSTWGRMWHFAYSVFLVLYGNSSL 60	
Qy	61 TAYGLVAGSVLVGATIGDAVIDKNARLYKAQTSLVYQNEVILGGITLMVFJHKEL 120	
Dp	61 TAYGLVAGSVLVGATIGDAVIDKNARLYKAQTSLVYQNSVILGGITLMVFJHKEL 120	
Qy	121 LTMHGKWLTCYLLITIANLANLASTATAATTIQDWTIVVAGEDRSKLANNATIRI 180	
DB	121 LTMHGKWLTCYLLITIANLANLASTATAATTIQDWTIVVAGEDRSKLANNATIRI 180	
Qy	181 DQTNILAPMAVGQIMTGSPIVGCFSQGNLVSMSVYLLKVVQKTPALAYKAGIKR 240	
DB	181 DQTNILAPMAVGQIMTGSPIVGCFSQGNLVSMSVYLLKVVQKTPALAYKAGIKR 240	
Qy	241 EEBTELKLNHHDTEPKPLETHLMLVYKDSNHEQETCASQMAEPRTRDGWY 300	
DB	241 EEBTELKLNHHDTEPKPLETHLMLVYKDSNHEQETCASQMAEPRTRDGWY 300	
Qy	301 SYNQPVPLAGMGLAFLYMTLGFDCTTGAYTOGLSISLNGASAITGTINGTVAF 360	
DB	301 SYNQPVPLAGMGLAFLYMTLGFDCTTGAYTOGLSISLNGASAITGTINGTVAF 360	
Qy	361 TWLRKCCOLVRTSLIGIAQLSCLLCTVTSYMPGSPLDLSSVPEDDIRSRPIQESITP 420	
DB	361 TWLRKCCOLVRTSLIGIAQLSCLLCTVTSYMPGSPLDLSSVPEDDIRSRPIQESITP 420	
Qy	421 TKPEITTEIYMNSNSANTVPEPSSEPVITISVSLFAGYTAARIQLWSFDLTVTQJL 480	
DB	421 TKPEITTEIYMNSNSANTVPEPSSEPVITISVSLFAGYTAARIQLWSFDLTVTQJL 480	
Qy	481 QENVIESSERGTINGVQNSMNYLIDLHFMVILAPNEAFGLVLISVSFAMGHIMYFR 540	
DB	481 QENVIESSERGTINGVQNSMNYLIDLHFMVILAPNEAFGLVLISVSFAMGHIMYFR 540	
Qy	541 FAQNTLGNKLPAQGPDAKEVRKENQANTSV 571	
DB	541 FAQNTLGNKLPAQGPDAKEVRKENQANTSV 571	
Result 4	Q9H19	

DR	GO:0006226	P:iron ion transport; IDA.
DR	IPR001993	Mitoch carrier.
DR	PROSITE; PS00215; MITOCH CARRIER; 1.	
SQ	SEQUENCE; 570 AA;	6270 MW; 7125CC6171394AOA CRC64;
Query Match	Score 89.4%; Best Local Similarity 90.2%; Matches 518; Conservative 18; Mismatches 31; Gaps 3;	Length 570;
Qy	1 MTRAGDNHRORGCCGSLADYITSAKFLLYGHSLSTWGDRMWHFAVSVELVLYGNSSL 60	Score 2618.5; Pred. No. 1.4e-195; Score 2618.5; Pred. No. 4.1e-195;
Db	1 MTKARDQTHOECGCSANLYTSAKFLLYGHSLSTWGDRMWHFAVSVELVLYGNSSL 60	Best Local Similarity 90.1%; Mismatches 18; Indels 7; Gaps 3;
Qy	61 TAVYGLVVAGSVLVGAIIIGDWKRNARTKVAQTSLVQVNSVTLCLGILMMYFLHKHEI 120	Query Match 89.2%;保守性 570 AA; Score 2612.5; DB 11; Length 570;
Db	61 TAVYGLVVAGSVLVGAIIIDWKNARTKVAQTSLVQVNSVTLCLGILMMYFLHKHEI 120	Best Local Similarity 90.1%; Pred. No. 4.1e-195;
Qy	121 LTMYHGWLWFLSCYIILITIANIANLASTATAITQDWVIVVAGEDERSKLLANNATIRR 180	Matches 517; Conservative 18; Mismatches 32; Indels 7; Gaps 3;
Db	121 LTMYHGWLWFLSCYIILITIANIANLASTATAITQDWVIVVAGEDERSKLLANNATIRR 180	Score 2612.5; DB 11; Length 570;
Qy	181 DOLTNILAPVAVGQINTFGSIVIGCFISGWNLVSMCVEYLMLKVYQOPTPALVAKLK 240	Best Local Similarity 90.1%; Mismatches 18; Indels 7; Gaps 3;
Db	181 DOLTNILAPVAVGQINTFGSIVIGCFISGWNLVSMCVEYLMLKVYQOPTPALVAKLK 240	Score 2612.5; DB 11; Length 570;
Qy	241 EETELKLQNLHKDTEPKPLEGTHLMGVKDSNTHELEHOEPTCASOMAEPFRTFRDGW 300	Query Match 89.2%;保守性 570 AA; Score 2612.5; DB 11; Length 570;
Db	241 VEESERKLQPLSKPDKTEPKPLEGTHMGEDSNIRELCQEPTASQAEPFRTFRDGW 300	Best Local Similarity 90.1%; Pred. No. 4.1e-195;
Qy	301 SYNNQPVFLAGMGLAFLYMVTFGEFCITGYAYTQGLSSSILSTMAGASAITGIMGTVAF 360	Matches 517; Conservative 18; Mismatches 32; Indels 7; Gaps 3;
Db	301 SYNNQPVFLAGMGLAFLYMVTFGEFCITGYAYTQGLSSSILSTMAGASAITGIMGTVAF 360	Score 2612.5; DB 11; Length 570;
Qy	361 TWLRKCGGLVRTGLLISGLAQQLSCLLICVSVMPGSPLDLSVSPEFDIERSRFIQGESITP 420	Best Local Similarity 90.1%; Mismatches 18; Indels 7; Gaps 3;
Db	361 TWLRKCGGLVRTGLLISGLAQQLSCLLICVSVMPGSPLDLSVSPEFDIERSRFIQGESITP 420	Score 2612.5; DB 11; Length 570;
Qy	421 -TKIPE--ITBEYMSNGNSNSANIVPETSPEPVLSVLISSVLLFAGVIAAIGLMSFDLTVT 476	Query Match 89.2%;保守性 570 AA; Score 2612.5; DB 11; Length 570;
Db	421 -TKIPE--ITBEYMSNGNSNSANIVPETSPEPVLSVLISSVLLFAGVIAAIGLMSFDLTVT 476	Best Local Similarity 90.1%; Mismatches 18; Indels 7; Gaps 3;
Qy	478 QLQENQVIESERGLINGVQNSMNYLLDLHFMVTLAPNEAFGLVLJLVSFVAMGHIM 537	Matches 517; Conservative 18; Mismatches 32; Indels 7; Gaps 3;
Db	478 QLQENQVIESERGLINGVQNSMNYLLDLHFMVTLAPNEAFGLVLJLVSFVAMGHIM 537	Score 2612.5; DB 11; Length 570;
Qy	538 YPRFAQNTLGNKLFAGPDAKEVRKENQANTSVV 571	Query Match 89.2%;保守性 570 AA; Score 2612.5; DB 11; Length 570;
Db	537 YPRFAQNTLGNQIFVGPDKEEVTDENQNPNTSVV 570	Best Local Similarity 90.1%; Mismatches 18; Indels 7; Gaps 3;
RESUL 5	Q9JKP4	SEQUENCE FROM N.A.
ID	Q9JKP4	PRELIMINARY;
AC	Q9JKP4;	PRT;
DT	01-OCT-2000 (TRMBLrel. 15, Created)	570 AA.
DT	01-OCT-2000 (TRMBLrel. 15, Last sequence update)	
DT	01-OCT-2003 (TRMBLrel. 25, Last annotation update)	
DE	Iron-regulated transporter, IREG1.	
GN	SLC40A1 OR SLC39A1 OR IREG1.	
Mus musculus (Mouse).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030;		
OC		NCBI_TaxID=10116;
OC		NCBI_TaxID=10116;
OX		NCBI_TaxID=10116;
RN		SEQUENCE FROM N.A.
RP		SEQUENCE FROM N.A.
RA		STRAINS-Sprague-Dawley;
RA		Yeh, K.-Y., Yeh, M., Glass, J.,
RA		"Iron induces ferroportin 1 (FPT1) clustering and redistribution in rat intestinal epithelial cells."
RT		rat intestinal epithelial cells."
RT		Submitted (FEB 2002) (TRMBLrel. 19, Created)
RT		01-JUN-2002 (TRMBLrel. 21, Last sequence update)
RT		01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE		Ferroportin 1.
DE		Rattus norvegicus (Rat).
OS		Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10030;
OX		NCBI_TaxID=10116;
RN		SEQUENCE FROM N.A.
RP		SEQUENCE FROM N.A.
RA		MCKIE A.T., MARCIANI P., ROITS A., BRENNAN K., WEHR K., BARROW D., MIRET S., BOMBAL A., FAREANEH F., HEDIGER M.A., HENTZ M.W., SIMPSON P.J., PETERS T.J., FARNAN H., FARNAN F., HEDIGER M.A., "A novel duodenal iron-regulated transporter, IREG1, implicated in the basolateral transport of iron to the circulation"; Mol. Cell 5:299-309(2000); DR; AF23110; AAFA429.1; -
RA		EMBL; AF394785; AAC77858.2; DR; GO; GO:0005743; C:mitochondrial inner membrane; IEA.
RA		MGI; MGID:1315204; Sci40aa.
RA		DR; GO:0006210; P:binding; IEA.
RA		DR; GO:0006210; P:transport; IEA.

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=1955;
 RN [1]
 RP SEQUENCE FROM N.A.
 Skuce C.;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AL731861; CAD61076.; -.
 DR NON_TER 1
 FT SEQUENCE 310 AA; 33727 MW; 0C2DFF6CECF051 CRC64;
 SQ 254 DTEPKPLIEGTHLMVKDSNINHEHQEPTCASQMAEPFRFRDGWSYNNOPVFLAGNG 313
 DB 3 NEP-SPEASQNM-----TSESEPDKTDGCYQMEPIRIPKQWAVNQSFFAAMS 55
 QY 314 LAFLYMTVLGFCCITGGAYATGGLSGSILSIMGASAATGMGTVAFTWLRKGCGLYRTG 373
 DB 56 LAFLYMTVLGFCCITGGAYATGGLSGSILSIMGASAATGMGTVAFTWLRKGCGLYRTG 115
 QY 374 LISGLAQSLCLLCSISVMEGSPLLSVSPEDRSRFQES---ITPTKPEITTE 429
 DB 116 FIAVTQQLSCLTICVASVERAARGSPFDLSVSPPEEV_LRHFGDGSRLREPTFIP-TTE 172
 QY 430 IIMSGNSNSANI-VPESSPESVPIISVSLI_PAGVAAARGIWSFOLTTQQLQNVISE 488
 DB 173 PPT-----QANVVPEPAPYEEPMVYVGLI_PAGVAAARVQWSFOLTTQQLQNVISE 227
 QY 489 RGTINGVONSNYYLDLHFMVILLAEPNAFLGLVLISSVFVANGHIMYFREAYKSLGS 548
 DB 228 RGVINGVONSNYYLDLHFMVILLAEPNAFLGLVLISSVFVANGHIMYFREAYKSLGS 287
 QY 549 KLF-A-CGPDAK 558
 DB 288 RLFFCSPDPQK 298

RESULT 14
 Q9NUSI PRELIMINARY: FRT: 167 AA.
 AC Q9NUSI_1
 DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 25, Last sequence update)
 DE Hypothetical protein FLJ1176.
 OS Homo sapiens (Human).
 EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; HOMO.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H., Nagatsuma M., Hosoi T., Kaku Y., Kodairi H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masubu Y., Niinomiya K., Iwayanagi T.;
 RA "NEDO human cDNA sequencing project.";
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK002038; BA92049.1;
 DR GO; GO:0005438; F:binding; IEA.
 DR GO; GO:0005810; P:transport; IEA.
 RT InterPro; IPR00193; Mitoch_carrier.
 DR PROSITE; PS00215; MIROCH_CARRIER; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 167 AA; 18252 MW; 8D391F5356733660 CRC64;

Query Match 29.3%; Score 859; DB 4; Length 167;
 Best Local Similarity 98.8%; Pred. No. 4.1e-59;
 Matches 165; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 266 MGYKDSNIHEHQEPTCASQMAEPFRFRDGWSYNNOPVFLAGMGIAFLYNTVLFDFD 325
 DB 1 MGYKDSNIHEHQEPTCASQMAEPFRFRDGWSYNNOPVFLAGMGIAFLYNTVLFDFD 60
 QY 326 CTTTGAYATGGTGSISIISIMGASAATGMGTVAFTWLRKGCGLYRTGSLGIAQLSCLJ 385
 DB 61 CTTTGAYATGGTGSISIISIMGASAATGMGTVAFTWLRKGCGLYRTGSLGIAQLSCLJ 120
 QY 386 LCIVSMPGSPLDLSVSPFEDIRSRIQGESITPTKIPRITTEYM 432
 DB 121 LCIVSMPGSPLDLSVSPFEDIRSRIQGESITPTKIPRITTEYM 167
 RESULT 15
 Q7Z4FB ID Q7Z4FB PRELIMINARY; PRT; 133 AA.
 AC Q7Z4FB; PRELIMINARY; PRT; 133 AA.
 DT 01-OCT-2003 (TREMBrel. 25, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DE MSTP019.
 GN MST079.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; HOMO.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RA Hui R.T., Zhao B., Sheng H., Qin B.M., Liu Y.Q., Liu B., Wang X.Y., Xu H., Zhang Q., Tong Y.X., Song L., Ji X.J., Liu B.H., Lu H., Chen J.Z., Cai M.Q., Zheng W.Y., Teng C.Y., Liu Q., Yu L.T., Lin J., Gong Q., Zhang A.M., Gao R.L.,
 RA "Homo sapiens normal aorta mRNA MST079.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF171087; AAQ13603.1; -;
 SQ SEQUENCE 133 AA; 14681 MW; 6D05FAEF993A6AA CRC64; -

Query Match 23.1%; Score 677; DB 4; Length 133;
 Best Local Similarity 99.2%; Pred. No. 4.7e-45;
 Matches 130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MTRADDHNQRGCGCSLADYLTSAKELLYLGHSLSTWDRMWHAFAVSFLVLYGNSSL 60
 DB 1 MTRADDHNQRGCGCSLADYLTSAKELLYLGHSLSTWDRMWHAFAVSFLVLYGNSSL 60
 QY 61 TAVGLVAGSVLVLGAIIGDWTDKNAFLKAQTSLVQNVSYLCCILMMVFLHKHEL 120
 DB 61 TAVGLVAGSVLVLGAIIGDWTDKNAFLKAQTSLVQNVSYLCCILMMVFLHKHEL 120
 QY 121 LMFMHGWLTS 131
 DB 121 LMFMHGWLTS 131
 Search completed: August 17, 2004, 18:04:57
 Job time : 46 secs